```
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                     December 22, 2003, 16:41:00 ; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec
                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                  1107863
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                             1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80522
ABB80525
ABB80526
ABB80559
ABB80563
ABB80564
ABB80565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80521
                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ü
                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                          US-09-909-164-10
                                                                                                            1 EEVVEXGMSYS (11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8333333333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           966.2
996.2
996.2
996.2
996.2
996.2
996.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                     Perfect score:
                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                    Database
                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26456786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
```

| • | | | | | | | | | | | |
|-----|------------|-----------------|-------|-----------|-----------------------|-----------|---------------------|----------------------------|---------|----------|------------|
| Alf | ۔ | ır | | 0 | 11 | 2 | ARB80567 | Henat | 4.1 | ain in | α |
| ž 8 | · | 11 50 | 96 | | 11 | 23 | ABB80568 | | 0 | C virus | |
| į | | 4 | | 3.5 | 11 | 23 | ABB80524 | Hebatit | 18 | • | 62 |
| | - | 4 | | 3.5 | 11 | 23 | ABB80528 | Hepatiti | 60 | • | 8 |
| | Н | 4, | | 3.5 | 11 | 23 | ABB80529 | Hepatiti | 8 | | Ø |
| | - | 4 | | 3.5 | 11 | 23 | ABB80561 | Hebatit | 100 | - | 60 |
| | rri | 4 | | 3.5 | 11 | 23 | ABB80562 | Hepati | 18 | C virus | CO. |
| | 1 | 4. | | 5.5 | 11 | 23 | ABB80523 | Hepatit | 18 | ζ. | 0 |
| | - | 4 | | 2. | 11 | 23 | ABB80527 | Hepati | tis | C virus | ш |
| | - | 4 | | 5.5 | 11 | 23 | ABB80535 | Hepati | _ | ζ, | 00 |
| | 2 | 4 | | 5.5 | 11 | 23 | ABB80536 | Hepatitis | 18 | C virus | 0 |
| | N | 4 | | 5.5 | 11 | 23 | ABB80539 | Hepatit | 118 | C virus | 89 |
| | 2 | 4 | | 5.5 | 11 | 23 | ABB80540 | Hepati | 118 | C virus | 60 |
| | 7 | 4 | | 5.5 | 11 | 23 | ABB80558 | Hepatiti | | C virus | 60 |
| | 7 | 4 | | | 11 | 23 | ABB80560 | Hepatitie | | 2 | 8 |
| | 7 | 4 | | 9. | 11 | 23 | ABB80544 | Hepati | _ | C virus | 8 |
| | ~ | 4 | | 9. | 11 | 23 | ABB80545 | Hepatiti | - | C virus | 100 |
| | 7 | 4 | | 9. | 11 | 23 | ABB80549 | Hepatitis | _ | C virus | 89 |
| | 7 | 4 | | 9.1 | 11 | 23 | ABB80552 | Hepatit | tis | C virus | ш |
| | 7 | 4 | | 9.1 | 11 | 23 | ABB80553 | Hepati | 8 | C virus | 60 |
| | e | 4 | | 8.(| 11 | 23 | ABB80530 | Hepatiti | 0 | - | 0 |
| | m | 4 | | 3.8 | 11 | 23 | ABB80538 | Hepatit | 118 | C virus | 00 |
| | m | 4 | | 3.8 | 11 | 23 | ABB80542 | Hepati | 118 | 7 | 00 |
| | m | 4 | | 8.8 | 11 | 23 | ABB80543 | Henaritis | _ | | |
| | 'n | 4 | | 6. | 1 | 23 | ABB80537 | Hepati | tis | - | |
| | | 4 | | | :- | 3 | ABB80541 | Henet | 1.0 | | 2 00 |
| | , (~ | 4 | | | : : | 3 | ABB80547 | Heret | 1 - | ; | |
| | , , | • 4 | | | 1 - | 3 6 | APPOOLA | Targett . | 0 0 | • | 0 0 |
| | י ה | • | | | 1: | ה ה | ADD00044 | nepari | 2 | | ם מ |
| | 1 (| * • | | , . | 1: | 2 6 | ABBROOSE | Hepart | 6119 | | י מי |
| | η. | 4. | - 1 | ٠ . د | Ξ: | 53 | ABBRUSSE | нераст | 118 | • | œ |
| | ₽' | ar · | 7 | 9. | Ξ: | 23 | ABB80557 | Hepati | t 18 | | 6 0 |
| | 4 | 4 | 7 | 6. | | 20 | AAU76810 | Hepati | itis (| • | 60 |
| | 4 | ₹' | 7 | 6.9 | 0 | 22 | ABG03621 | Novel | human | - | 8 |
| | 4 | 4 | 7 | • | 1022 | 22 | ABG05826 | Novel | human | - | 6 |
| | 4 | 4 | 7 | 6.5 | 0 | 22 | ABG08173 | Novel | human | | 0 |
| | 4 | ٣ | 7 | 5.0 | 11 | 23 | ABB80546 | Hepati | itis | | ß |
| | | | | | | | | | | | |
| | | | | | | | ALIGNMENTS | | | | |
| | | | | | | | | | | | |
| | | | | | | | | | | | |
| | RESULT | 1 6 | | | | | | | | | |
| | 200 | | | 9 | | | | | | | |
| | | ABB80521 | scano | standard; | peptide; | | 11 AA. | | | | |
| | | ARROG21. | | | | | | | | | |
| | | | | | | | | | | | |
| | | 08-OCT-20 | 002 | (first | t entry) | ^ | | | | | |
| | | • | | | | | | | | | |
| | | Hepatitis | U | virus h | NS3/NS4a | | serine protease | inhibitor peptide | #1. | | |
| | | Honotitio | C | . 01.01 | . 727 | orino | 00000 | inhihitor. alaba-korosmide | i ii | | |
| | | vi me ide. | j | , , | , | 1 1 0 | לקים הפמפה ל | | Callit | ָ ט | |
| | | | | | | | | | | | |
| | S | Synthetic | | | | | | | | | |
| | | ; | | • | | ç | | | | | |
| | , | Key Wodifiod | 4 | ğ. | Location/Qualiti 1 | /gra | lilers | | | | |
| | | - DOLLINON | פדרם | , È | " aton | N-t-N | "N-terminal acetyl" | | | | |
| | | Modified- | -Bite | 9 | | : | - 10000 | | | | |
| | | | | /n | note= " | "Norvalyl | carbonyl | forming keto-amide | linkage | age with | ц |
| | | 7 | | , | | residue | 7" | | | | |
| | E | Modified-site | Bite | 11 | 1 | | | | | | |
| | Ē | | | | | , | | | | | |

1

```
virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                ABB80525;
                                                                                                                                                                                                                                                                                                             virucide.
                                                                                                         Sequence
                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                셤
                                                                                                                                                                                                                      ö
                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                      pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
                                                                                                                                                                                                                      ö
                                                                                                                                                                                           , DB 23; Lens.
0. 0.0013; Indels
                                                                                                                                                                                                    Length 11;
                                                                                                                                                                                             96.2%; Sco...
100.0%; Pred. No. v...
'... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunck TK;
                   Ä
                                                                                                                                                                                                                                                                                                       ABB80522 standard; peptide; 11 AA.
                                                                                          Claim 17; Page 64; 69pp; English.
                    Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                                                 96.4
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                         1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                         EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lim-wilby M, Levy OE,
(CORV-) CORVAS INT INC
                    Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-361643/39.
                                    WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                   11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                        virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                          08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                        ABB80522;
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                       virucide
                                                                                                                                                                                                                                                                                     RESULT 2
                                                                                                                                                                                                                                                                                              ABB80523
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                         g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of
                                                The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                          96.2%; Score 50; DB 23; Length 11;
100.0%; Pred. No. 0.0013;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 64; 69pp; English.
Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80525 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.vv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
                                                                                                                                                                                                                                                                                       11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-2002
```

Length 11;

```
Query Match
Best Local Similarity
                                                                                                                                    ABB80559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity
                                                                                               RESULT 5
                                                                 셤
                                                                                                                                    ઠ
                                                                                      ö
         a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                          "Norvalyl carbonyl forming keto-amide linkage with
                                                                                      Gaps
                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
                                                                                      ö
                                                                                     IndelB
                                                                   Length
                                                                  DB 23; Le
0.0013;
hes 0;
                                                                 96.2%; Score 50; DB 100.0%; Pred. No. 0.0 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                       'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                         'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                       "D-form residue"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    residue 7"
                                                                                                                                                                        ABB80526 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                (first entry)
                                                                           Local Similarity 100.
es 11; Conservative
                                                                                                       1 EEVVPXGMSYS 11
                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lim-wilby M, Levy OE,
                                                                                                                     EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-361643/39.
                                                11 AA;
                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                                                                                                                                                                                  Synthetic.
                                                 Sequence
                                                                   Query Match
                                                                                                                                                                                                                                                                virucide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                           Best Loc
Matches
                                                                                                                                                      RESULT 4
                                                                                                                                                                ABB80526
           ន្តដ្ឋប្បន្នន
                                                                                                                         셤
                                                                                                        ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ingredient
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compound having hepatitis C virus protease inhibitory
al for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical composition comprising the peptide as an active ingite useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39
                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
DB 23; Le...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.2%; Score 50; DB 23; Length 11 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels
                Score 50; DB 2
Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
96.2%; Sc.
100.0%; Prer
0; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunck TK;
                                                                                                                                                                                                                                    ABB80559 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                      Conservative
                                                                                             11
                                                                                                                                   1 REVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORV-) CORVAS INT INC
                                                                                               EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lim-wilby M,
                                                                                                                                                                                                                                                                                                                    08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
```

ABB80563;

RESULT

셤

virucide

```
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                            /note= "Leucyl carbonyl forming keto-amide linkage with residue 7"
                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a peptide compound of the invention having
               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.2%; Score 50; DB 23;
100.0%; Pred. No. 0.0013;
tive 0; Mismatches 0;
                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1
                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB80565 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                   19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 REVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AA;
                                                                                                                                                                                                                                                                                 WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                 Key
Modified-site
                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-2002
                                                                                                                                                                                                                                                                                                                  31-JAN-2002
                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                    carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 11;
0.0013;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                   'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                     11
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.2%; Score 50;
100.0%; Pred. No.
:ive 0; Mismatcl
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŢĶ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB80564 standard; peptide; 11 AA.
                                                                                   ABB80563 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                   /note= "Valyl ca
residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100 tes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
   1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200208251-A2
                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-2002
                                                                                                                                                   08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 11
```

ö

Gaps

ABB80564;

RESULT 7 **ABB80564**

ò

Sequence

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "(s,s)allothreonyl carbonyl residue forming a
keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47
                                                                                                                                                                                                                                                                                                                                                                                                                                     96.2%; Score 50; DB 23; Length 11; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "C-terminal amide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŢĶ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80567 standard; peptide; 11 AA
                                                                                                                                                                                                                                          Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brunck
                19-JUL-2001; 2001WO-US23169.
                                              21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                         96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                OE,
                                                                                (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||||||||||||||||EEVVPXGMSYS
                                                                                                                                              WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-361643/39
                                                                                                                Levy
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         11 AA;
                                                                                                                                                                                                            virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                              Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80567;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketomide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    armaceutical composition comprising the peptide as an active ingredient useful for treating disorders associated with hepatitis C virus.
                              /note= "Norleucyl carbonyl forming keto-amide linkage
    with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                      peptide compound having hepatitis C virus protease inhibitory ty useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "2-aminoisobutyryl carbonyl residue forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Le
. 0.0013;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.2%; Score 50; DB 100.0%; Pred. No. 0.0.1 ive 0; Mismatches
/note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "N-terminal acetyl"
                                                                              "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
/note= "C-terminal amide"
                                             with residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                        ŢĶ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą.
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                          Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80566 standard; peptide; 11
                                                                                                                                                                          19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                        21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEVVPXGMSYS 11
                                                             11
/note=
                                                                                                                                                                                                                                                                        Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                        WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AA;
                                                                                                                                                                                                                                                                                                                                                                        virus protease
                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200208251-A2
               Modified-site
                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                      Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-2002
                                                                                                                                            31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                       activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80566,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

Matches

셤

ò

Novel

ö

Gaps

```
σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                              11 AA;
                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lim-wilby M,
                                                                                                                                                                                                                  08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                               ABB80524;
                                                                                                                                                                                                                                                                   virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                     ន្តដ្ឋប្បទ្ធប្អន្ត
                                                                                                                           셤
                                                                                                         ઠે
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have
                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Alpha-propynyl-glycinyl-carbonyl residue forming
a keto-amide linkage with residue 7"
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C
       peptide compound having hepatitis C virus protease inhibitory
tty useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
                                                                                                                                                                                       o;
                                                                                                                                                                  Length 11;
                                                                                                                                                                                       Indels
                                                                                                                                                                                     ö
                                                                                                                                                                  96.2%; Score 50; DB 23; 100.0%; Pred. No. 0.0013;
                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
/note≈ "C-terminal`amide"
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunck TK;
                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; 69pp; English.
                                               English.
                                                                                                                                                                                                                                                                             standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                     11; Conservative
                                               Claim 17; Page 65; 69pp;
                                                                                                                                                                                                        1 EEVVPXGMSYS 11
                                                                                                                                                                                                                            EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-361643/39.
                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                              11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page
                             virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lim-wilby M,
                                                                                                                                                                                                                                                                                                                   08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                ABB80568;
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                             ABB80568
                                                                                                                                                                                                                                                                                                                                                                   virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity
                   activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel
         Novel
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                          RESULT 11
ò
                                                                                                                                                                                                                            셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forming keto-amide linkage with
                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #4
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 11;
                                                                                                                                                                                  Length 11
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                  DB 23;
0.0013;
                                                                                                                                                                                  Score 50; DB 2
Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Norvalyl carbonyl residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck TK;
                                                                                                                                                            96.2%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB80524 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                      1 REVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-361643/39
```

Matches

ઠે

g

ABB80528 ABB80528;

RESULT 13 ABB8052 virucide

```
"Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 23; Length 11;
Pred. No. 0.0088;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                    "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                   note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                'note= "D-form residue"
                                                                                                                                                                                                                                                Location/Qualifiers
                                  ABB80529 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.06
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guery Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EBVVPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AA;
                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lim-wilby M,
                                                                                                 08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                                                                                                                  Synthetic.
                                                                  ABB80529;
                                                                                                                                                                                 virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80561
                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BXXX
                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 23; Length 11;
Pred. No. 0.0088;
0; Mismatches 1; Indels
                  Indela
 Pred. No. 0.0088;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.5%;
90.9%;
Similarity 90.9%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                 1 EEVVPXGMSYS 11
                                                                              EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||||||||
EEVVPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                             08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                Synthetic.
```

ö

Gaps

ö

Sequence Query Match

Best Loc Matches

8 q ABB80561;

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                             /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 23; Length 11;
Pred. No. 0.0088;
0; Mismatches 1; Indels
                                                                                                                                                   'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                              /note= "C-terminal amide"
                                                                                                                                                                                                                       'note= "D-form residue"
                                                                                                                                                                                                                                                  'note= "Oxymethionine"
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                               19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2000; 2000US-220101P.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-361643/39.
                                                                                                                                                                                                           œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AA;
                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus protease
                                                                                                                                                                                                                                                                                                         WO200208251-A2
                                                                                                                          Key
Modified-site
                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                               Modified-site
08-OCT-2002
                                                                                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
```

1 EEVVPXGMSYS 11 1 EEVVPXGMDYS 11 ò a

..

ö

Gaps

ö

Search completed: December 22, 2003, 17:41:01 Job time : 33.4667 secs

23

Tue Dec

```
Sequence 73, Appl
Sequence 7885, Ap
Sequence 236, App
Sequence 236, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 236, App
Patent No. 5177197
Patent No. 5177197
Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                              December 22, 2003, 16:37:03; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 66,
Sequence 66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence (
Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents AA:*
: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-228-986-73
US-09-328-322-7885
US-08-637-7985-236
US-08-637-7598-236
US-09-201-945-236
S177197-1
5177197-30
US-09-521-656-66
US-08-86-23
US-08-86-23
US-08-86-377-2
US-08-86-377-2
US-08-86-377-2
US-08-86-361-2
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-464-517-6
US-08-463-772-6
US-08-246-361A-4
                                                                                                                                                                                                                                                                                                                              328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                      US-09-909-164-10
52
1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244

461

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

1001

10
                    Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                Sequence:
                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š.
```

```
Sequence 788; Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
                                                                                                                                                                                                                                                                                                                        APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REPERRICE: 11000/1020
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                        Appl
Appl
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                   Sequence Sequence Sequence S
                                                                             Sequence Sequence S
                                                                                                               Sequence Sequence Sequence
                                                                                                                                                   Sequence
                                                                                                                                                                          Sequence
          Sequence
                                                                                                                                                                                                 Seguence
                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 4; Length 947;
Pred. No. 1.3e+02;
2; Mismatches 1; Indels
                   US-08-464-517-23
US-08-246-361A-6
US-08-246-361A-23
US-08-246-361A-23
US-08-247-120-8
US-08-460-694-2
US-08-464-517-20
US-08-246-361A-19
US-08-246-361A-19
US-08-246-361A-19
US-08-246-361A-19
US-08-246-361A-19
US-08-246-361A-19
US-08-246-361A-19
US-08-246-361A-19
US-08-246-361A-19
US-08-463-772-19
PCT-US93-05000-4
PCT-US93-05000-6
                                                                                                                                                                                  US-08-460-744-2
US-07-667-711B-2
                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                         Sequence 73, Application US/09228986 Patent No. 6359198 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT

ORGANISM: Pinus radiata
US-09-228-986-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:||:||
686 VMPSGISYS 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMSYS 11
 US-09-328-352-7885
                                                                                                                                                                                                                                                                              US-09-228-986-73
 RESULT 1
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

ö

Gaps

ö

Similarity 66.7%; Pred. No. 2.1e+02; Similarity 66.7%; Pred. No. 2.1e+02; 6; Conservative 2; Mismatches 1; Indels

Query Match Best Local Similarity Matches 6; Conserv

; TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-7885

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 3; Length 45;
Pred. No. 6.6;
1; Mismatches 3; Indels
                          COMPUTER READABLE FORM:
MEDLIUM TYPE: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY disk
COMPUTER: DAMPE PLODS/MS-DOS
SOFFWARE: PREADINI Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: UD-BC-1997
CLASSIFICATION NUMBER: PCT/GB95/02875
FILING DATE: UD-BC-1995
CLASSIFICATION NUMBER: 31,284
FILING DATE: 1.1-DEC-1995
CLASSIFICATION NUMBER: 31,284
REPERRINGFORCET UNMBER: RPMS 101 CON
TELECOMMUTICATION NUMBER: 31,284
REPERRINGFORCET UNMBER: RPMS 101 CON
TELECOMMUTICATION NUMBER: RP995
INFORMATION OF SEQ 1D NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KESULI 5945-236

Sequence 216, Application US/09201945

Sequence 216, Application US/09201945

Patent No. 6342216;
GARBAL INFORMATION:
FAPPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1201 West Peachtree Street
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
INFOLIATION OF STEEN: PC-DOS/NS-DOS
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PATENTION SYSTEM: PC-DOS/NS-DOS
SOFTWARNT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0°
"---hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 REVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ERISPLGWSY 10
Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-871-355A-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
RICH APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PABEL, Patera L.
REGISTRATION: NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION NUMBER: RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-871-355A-236

Sequence 236, Application US/08871355A

Patent No. 6015669

GENERAL INFORMATION:

APPLICANT: David William Holden

ITLE OF INVENTION: Identification of Genes

NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street
                                                                                                           RESULT 3
US-08-637-759B-236
Squence 236, Application US/08637759B
Squence 236, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 2
Pred. No. 6.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||| |:|:
596 EVVPEGLSF 604
  2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-637-759B-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
    ઠ
                                             g
```

Gapa

```
US-09-521-650-66; Sequence 66, Application US/09521650; Batent No. 6335429; GENERAL INFORMATION: APPLICANT: Weber, Eckard; APPLICANT: Gai, Sui Xiong; APPLICANT: Cai, Sui Xiong; APPLICANT: Cai, Sui Xiong; APPLICANT: Drewe, John F.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%;
50.0%;
                                                                                                                                                                                                                                                                                             63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  399 KBICPGGMGYT 409
                                                                                                                                                                                                                                                                                                                                                            1 REVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 BEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DDIVPCSMSY 10
                                                                                                                                                                                                                                             LENGTH: 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
                                                                                                                                                                                                                                                            5177197-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                            윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
517197-51
FACENT NO. 517197
HEALDAR: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
HERDIT, CHRISTER;HELLMAN, ULP;MIYAZONO, KOHEI;CLAESSON-WELSH,
LENA;HELDIN, CARL-HENRIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWITH FACTOR-BETA1-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
HELDING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATENT NO. 5177197

PAPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

WENNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,

JLENSTEDIN, CARL-HERIKI

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING

HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA:

RELING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 6; Length 65;
Pred. No. 10;
                                                                                                                                                                                                                                                              Score 33; DB 4; Length 45; Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 6
Pred. No. 81;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                  1; Mismatches
                                RPMS 101
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEPAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%;
                                                                                                                                                                                                                                                                 63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 45.5
Best Local Similarity 45.5
                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.5
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|: | || |:
399 KEICPGGMGYT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|: | || |:
52 KBICPGGMGYT 62
                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 410
                                                                                                                                                                                                                        US-09-201-945-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5177197-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
5177197-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5177197-1
                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
NENDET STATES AND STAT
```

APPLICANT: Zhang, Han-Zhong

```
| Sequence 23, Application US/08580988A
| Patent No. 5856161
| GENERAL INFORMATION:
| APPLICANT: Aggarwal et al.
| TITLE OF INVENTION: Tumor Necrosis Factor
| TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
| TITLE OF INVENTION: For Its Use
| NUMBER OF SEQUENCES: 27
| CORRESPONDENCE ADDRESS:
| ADDRESSER: Dr. Benjamin A. Adler
| STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.5%; Score 32; DB 2; Length 102; 60.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ABDES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER: READBLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRATING DATE: January 3, 1996
CLASSIFICATION UNMERE: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFICATION DATA:
APPLICATION UNMERE:
FILING DATE: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       713-777-6908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 EEVPPLAMNY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: no
PRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                        US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-08-460-694-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/0916888

Fater No. 6342611
GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Cain, Sui Xiong
APPLICANT: Cain, Sui Xiong
APPLICANT: Cain, Sui Xiong
TITLE OF INVENTION: No. 6342611e1 Fluorogenic or Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescence TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the TITLE OF INVENTION: Use Thereof EILE REFERENCE: 1735.0290002 CURRENT APPLICATION WUMBER: US/09/521,650 CURRENT APPLICATION WUMBER: 09/168,888 EARLIER FILING DATE: 1998-10-09 EARLIER FILING DATE: 1998-10-09 EARLIER FILING DATE: 1998-10-09 EARLIER FILING DATE: 1998-10-00 EARLIER FILING DATE: 1998-03-03 NUMBER: US 69/033,661 EARLIER FILING DATE: 1998-03-03 NUMBER OF SEQ ID NOS: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic; CTHER INFORMATION: Peptide US-09-168-888-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.9; 2; Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DDIVPCSMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DDIVPCSMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 BEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-521-650-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-168-888-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 66
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 66
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
```

ઠે g ö

Gaps ö

3; Indels

ò 셤

```
Gapa
                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                     Score 32; DB 3; Length 152;
Pred. No. 42;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 3; Length 152;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ARNOLD: ANDREW
TITLE OF INVENTION: Pradi Cyclin and Its cDNA
TITLE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSES: STEERT: ADDRESSES: STEERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER: Eloppy disk

COMPUTER: Eleppy disk

COMPUTER: Eleppy disk

COMPUTER: Eleppy disk

COMPUTER: DarentIn Release #1.0, Version #1.30

COMPUTER: PatentIn Release #1.0, Version #1.30

COMPUTER: DarentIn Release #1.0, Version #1.0, Version #1.30

COMPUTER: DarentIn Release #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 22, 2003, 16:43:43
Job time : 10.1333 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-07-667-711B-4
; Sequence 4, Application US/07667711B
; Patent No. 6110700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%;
60.0%;
                                                                                                                                                                              61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                             Query Match
Best Local Similarity 60.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                p TOPOLOGY: linear
p MOLECULE TYPE: peptide
US-08-460-744-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide
US-07-667-711B-4
                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                  20 EBVPPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 BEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-00-460-744-4

1S Sequence 4, Application US/08460744

1 Sequence 8. 6107541

2 GENERAL INFORMATION:
ATITLE OF INVENTION: PRADI Cyclin and its CDNA
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSS:
ADDRESSEE: STRENE, RESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
STATE: DC
COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 2; Length 152;
Pred. No. 42;
1; Mismatches 3; Indels
                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPSY disk
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 425
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 0609.4070002
TELEFRAM: 202-371.2600
TELEFAX: 202-371.2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCONCATNY, EVELYN H.
REGISTRATION NUMBER: 35,279
REFERENCE/POCKET UNBER: 35,279
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relev:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-460-694-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 REVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 EEVFPLAMNY 29
DC
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

```
December 22, 2003, 16:40:14 ; Search time 20.8667 Seconds (without alignments) 98.451 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/DEMEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             696363 seqs, 186758610 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Applications AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                          US-09-909-164-10
52
1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                              Title:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | d | | | | | | |
|---------------|-------|----------------|--------------------------|----|---------------------|-------------|----------|--|
| Result No. | Score | Query Match | Query Match Length DB | 08 | ai Gi | Description | | |
| - | 38 | 73.1 | [| 12 | US-10-029-120-4 | Seguence 4 | Appli | |
| 7 | 38 | 73.1 | | 14 | US-10-027-806-4 | Sequence 4 | i, Appli | |
| , 3 | 38 | 73.1 | | 14 | US-10-034-623-4 | Sequence 4 | i, Appli | |
| 4 | 38 | 73.1 | 3472 | 15 | US-10-027-801-4 | Sequence 4 | i, Appli | |
| Ŋ | 36 | 69.2 | | 12 | US-10-029-386-32486 | | 32486, A | |
| 9 | 35 | 67.3 | | 12 | US-10-029-386-32076 | Sequence 3 | 32076, A | |
| 7 | 34 | 65.4 | | 12 | US-10-094-749-2565 | Sequence 2 | 2565, Ap | |
| 80 | 34 | 65.4 | | 15 | US-10-101-464A-73 | | 73, Appl | |
| σ | 34 | 65.4 | | 12 | US-10-122-067-4 | | 4, Appli | |
| 10 | 34 | 65.4 | | 12 | US-10-096-534-67 | Sequence 6 | 7, Appl | |
| 11 | 34 | 65.4 | | 12 | US-10-122-067-2 | Sequence 2 | 2, Appli | |
| 12 | 33 | 63.5 | 66 | 15 | US-10-106-698-7477 | Sequence 7 | 7477, Ap | |
| 13 | 33 | 63.5 | | 15 | US-10-214-766-43 | Sequence 4 | 13, Appl | |
| 14 | 33 | 63.5 | | 11 | US-09-992-600A-108 | Sequence 1 | 108, App | |
| 15 | 33 | 63.5 | 47B | 11 | US-09-924-340-108 | Segmence 1 | OB. App | |

| Sequence 184, App Sequence 108, App Sequence 108, App Sequence 108, App Sequence 108, App Sequence 108, App | 3010 26, 130, 261, 66, | 53.024 | Sequence 4, Appli Sequence 4, Appli Sequence 275, App Sequence 1061, Ap Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli | 1036 467 878 878 14, |
|--|---|---|---|--|
| 11 US-09-746-783-184 12 US-09-992-095B-108 12 US-10-154-678-108 15 US-10-000-489-108 15 US-10-000-986-108 | 12 US-10-094-749-3010 11 US-09-820-843A-26 16 US-10-080-170-130 12 US-10-116-275-261 10 US-09-947-389-66 12 US-10-138-375-66 | 12 US-10-199-820-241 12 US-10-094-749-2076 12 US-10-094-748-23 12 US-10-116-275-114 13 US-09-919-497-54 | 14 US-10-024-086-2 14 US-10-024-066-4 12 US-10-116-275-275 10 US-09-925-300-1061 9 US-09-923-304-4 15 US-10-101-921-4 | 9 US-09-815-242-10384 12 US-10-287-274-467 14 US-10-151-736-4 10 US-09-764-847-878 15 US-10-092-154-878 10 US-09-948-080-14 |
| 4444478 87444 8744 874 | 648 653 1152 1394 10 | 244 244 244 244 286 | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 1377 1377 2799 53 53 59 |
| 68 68 68 68 68 68 68 68 68 68 68 68 68 6 | 63.5 63.5 63.5 61.5 61.5 | 611.5 611.5 611.5 | 6115 6115 6115 6115 6115 6115 6115 6115 | 61.5 61.5 61.5 59.6 59.6 |
| | 22233333333333333333333333333333333333 | 22222 | 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | 32 32 31 31 31 |
| 16 117 119 20 21 | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | , w w w w w u 4 ti 0 t 0 0 | 4 4 4 4 4 0 4 4 6 4 8 |

ALIGNMENTS

```
Sequence 4. Application US/10029120
; Sequence 4. Application US/10029120
; Publication No. US20030175708A1
; GRENERAL INFORMATION:
    APPLICANT: Swanson, Rohard V.
; APPLICANT: Swanson, Rohard V.
; APPLICANT: Schleper. Christa
; TILLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DOORP.002A
; CURRENT PILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: LARLER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: BARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FREESE for Windows Version 3.0
; FROM A 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.1%; Score 38; DB 12; Length 3472; 54.5%; Pred. No. 1.6e+02; ive 4; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10027806
Publication No. US20020160476A1
GENERAL INFORMATION:
APPLICANT: Swanson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|:| |:|
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.1
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-027-806-4
RESULT 1
US-10-029-120-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-029-120-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

```
LENGTH: 3472
    SEQ ID NO 4
                                                                                                                                                                                                                                                                           윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Scaleper, Christa
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERRNCE: DCORP. 002A
CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10027801
Publication No. US20030054364A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT PILING DATE: 2001-12-21
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLBIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.0024
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR PILING DATE: EARLIER PILING DATE: 1999-09-29
SOFTWARE: RABLIER FILING DATE: 123
SOFTWARE: RABLIER FILING DATE: RESC for Windows Version 3.0
SEQ ID NOS: 123
SOFTWARE: PASTSC for Windows Version 3.0
LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                             Score 38; DB 14; Length 3472;
Pred. No. 1.6e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 14; Length 3472;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10034623
Publication No. US20020198365A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
                                                                                                                                                                                                                                                                                                                                                Ouery Match 73.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:| |:|:|
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|:| |:|:|
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-034-623-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-10-027-801-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-034-623-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
Sequence 32076. Application US/10029386

Publication No. US20330194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HANDEN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: WHORER US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vere: 1.1
SEQ ID NO 32076
                                                                                                                                                                                                                                                                                                                                                                                                                              **Sequence 32486, Application US/10029386

**; Sequence 32486, Application US/20030194704A1

**; Publication No. US20030194704A1

**; Publication No. US20030194704A1

**; Publication No. US20030194704A1

**; Publicant: Penn, Sharron G.

***APPLICANT: Rank, David R.

**; APPLICANT: Hanzel, David R.

**; APPLICANT: Hanzel, David R.

**; TITLE OF INVENTION: HUMMA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMMA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION UNMER: US/10/029,386

**CURRENT APLICATION UNMER: US/10/029,386

**CURRENT FILING DATE: 2001-12-20

**NUMBER OF SEQ ID NOS: 34288

**SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

**SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

**SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                      ö
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                   Length 3472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.2%; Score 36; DB 12; Length 153; 70.0%; Pred. No. 12; tive 1; Mismatches 2; Indels
                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: MAP TO AF002994.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
                                                                                                                   Score 38; DB 15;
Pred. No. 1.6e+02;
4; Mismatches 1;
TYPE: PRT; CENARCHAEUM SYMDIOSUM; ORGANISM: CENARCHAEUM US-10-027-801-4
                                                                                                                      Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                |:|:| |:|:|
2294 BDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                1 REVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 REVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo Bapiens
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-10-029-386-32486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-029-386-32486
```

```
APPLICANT: Strabala, Timothy
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.102002
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT APPLICATION NUMBER: US/200-01-01
PRIOR PLILNG DATE: 1999-01-01
PRIOR PLILNG DATE: 1999-01-01
PRIOR PLILNG DATE: 1999-11-01
PRIOR PLILNG DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 989
SSO ID NOS: 989
SSO ID NO 73
LENGTH: 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 67, Application US/10096534
Publication No. US20030166887A1
Publication No. US20030166887A1
Publication No. US20030166887A1
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Yates, Karen
APPLICANT: Mill APPLICANT: APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.4%; Score 34; DB 12; Length 1163; 72.7%; Pred. No. 3.1e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.4%; Score 34; DB 15; Length 947; 66.7%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10122067
Publication No. US20030165883A1
GENERAL INFORMATION:
APPLICANT: Rory A.J. Curtis
ITILE OF INVENTION: 27091, A PHOSPHOLIPID TRANSPORTING
ITILE OF INVENTION: 27091, A PHOSPHOLIPID TRANSPORTING
ITILE OF INVENTION: 27091, A PHOSPHOLIPID TRANSPORTING
CURRENT APPLICATION NUMBER: US/10/122,067
CURRENT PILING DATE: 2002-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PLING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.56+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||| | | |
133 EEVVPRGGSVS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 BEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                686 VMPSGISYS 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-101-464A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-096-534-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-122-067-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-122-067-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                            Score 35; DB 12; Length 236; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%; Score 34; DB 12; Length 290;
66.7%; Pred. No. 66;
ive 2; Mismatches 1; Indels
; OTHER INFORMATION: MAP TO 298050.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.3
US-10-029-386-32076
                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NACHHARI, KENNI
APPLICANT: MACHHARI, KENNI
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
FRIOR FILING DATE: 2002-01-24
FRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VOYEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2565, Application US/10094749
Publication No. US20030219741A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-10-101-464A-73
; Sequence 73, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                            67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 WPAGLTYS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:|| |:|
EEIVPMGIS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMS 9
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-094-749-2565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2565
LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                         COCATION: (40)—
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_PRATURE
COCATION: (57)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (58)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
NAME/KEY: MISC_FEATURE
                                                                          LOCATION: (3) —
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (13)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COCATION: (65)—
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAMEA/KEY: MISC_PEATURE
LOCATION: (82)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAMEA/KEY: MISC_PEATURE
LOCATION: (93)
                                                                                                                                                                                                                                                                                    LOCATION: (39)—
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE

    i LOCATION: (93)
        Ormer INFORMATION: Xea equals any of the naturally occurring L-amino acids
US-10-106-698-7477

                                                                                                                                                                                                                 LOCATION: (14) -
OTHER INPORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-214-766-43

Sequence 43, Application US/10214766

Publication No. US20030084473A1

GENERAL INPORMATION:

APPLICANT: Gocal, Greg

TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS

PILE REPERENCE CA138

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US/10/214,766

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,734

PRIOR FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.2

1 ENGINE OF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 15; Length 426;
Pred. No. 1.6e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 33; DB 15; Length 99;
; Pred. No. 32;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.5
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 EFVIPAGQSY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMSY 10
       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|| |:|||
73 LVPVGISYS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-214-766-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide FILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide FILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-01-03

PRIOR FILING DATE: 1999-01-03

NUMBER OF SEQ ID NOS: 8544

SOFTWARE: PATENTI VET. 3.0
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 12; Length 1499;
Pred. No. 4.2e+02;
0; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                  Score 34; DB 12; Length 1499;
Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10122067
Publication No. US20030165883A1
GENERAL INFORMATION:
THE OF INVENTION: 27091, A PHOSPHOLIPID TRANSPORTING
TITLE OF INVENTION: 27091, A PHOSPHOLIPID TRANSPORTING
TITLE OF INVENTION: ATPASE MOLECULE AND USES THEREFOR
TITLE REFERENCE: MPIOL -05891R
CURRENT APPLICATION NUMBER: US/10/122,067
CURRENT FILING DATE: 2002-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRESERG for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
FILE REPERENCE: B0801/7244/KA/ERP
CURRENT APPLICATION NUMBER: US/10/096,534
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US 60/274,980
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7477, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.4%;
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            469 EEVVPRGGSVS 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 EEVVPRGGSVS 479
                                                                                                                                                                                                                                                                                                                                                                                                               1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 BEVVPXGMSYS 11
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-122-067-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-106-698-7477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 1499
TYPE: PRT
                                                                                                                                                                     SEQ ID NO 67
LENGTH: 1499
                                                                                                                                                                                                                                                                   US-10-096-534-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7477
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-924-340-108

US-09-924-340-108

Sequence 108, Application US/09924340

Publication No. US20030027248A1

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US2.REG

CURRENT PILING DATE: 2001-08-06

PRIOR PRIOR PRILICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-15

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/298,698

PRIOR PRILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112

SOFTWARE: JPAtent

SEQ ID NO 108

LENGTH: 478

LENGTH: 478
                                                                                                                           APPLICANT: Benjain, Stephane
APPLICANT: Banaka, Hiroaki
TILB OF INVENTION: HUMAN CONAS AND PROTEINS AND USES THEREOF
FILE REPERENCE: 91.U54 DIV
CURRENT FILING DATE: 2001-11-13
FRICA APPLICATION NUMBER: US 09/924,340
PRIOR PLILNG DATE: 2001-08-06
PRIOR PLILNG DATE: 2001-08-05
PRIOR PLILNG DATE: 2001-06-29
PRIOR PLILNG DATE: 2001-06-29
PRIOR PLILNG DATE: 2001-06-25
PRIOR PLILNG DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.5%; Score 33; DB 11; Length 478; Best Local Similarity 60.0%; Pred. No. 1.9e+02; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.5%; Score 33; DB 11; Length 478; Best Local Similarity 60.0%; Pred. No. 1.96+02; Matches 6; Conservative 1; Mismatches 3; Indels
                               Sequence 108, Application US/09992600A Publication No. US20030027161A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 EVAPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-600A-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-924-340-108
US-09-992-600A-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
Qy 2 EVVPXGMSYS 11
|| | | ||:
Db 239 EVAPAGASYN 248
```

Search completed: December 22, 2003, 17:32:42 Job time: 20.9333 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

December 22, 2003, 17:24:36; Search time 9.06667 Seconds (without alignments) 116.675 Million cell updates/sec Run on:

US-09-909-164-10 52 1 BEVVPXGMSYS 11 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 76:*
1: Dirl:*
2: Dir2:*
3: Dir3:*
4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| IES | Description | hypothetical 367K | probable sulfate p | sulfate permease - | V1 protein - tobac | DNA segregation AT | | | zinc finger protei | topoisomerase IV s | DNA-binding protei | hypothetical prote | cell division inhi | probable ABC subst | hypothetical prote | 50S ribosomal prot | hypothetical prote | | _ | hypothetical prote | beta-ketoacyl-ACP | hypothetical prote | | cdc37 protein - fi | iron(III) ABC tran | - pacteriocin BCNS | ATP-dependent DNA | ш, | grov | DNA-directed RNA p |
|-----------|----------------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|-------------------|--------------------|--------|--------------------|--------------------|--------------------|-------------------|--------|------|--------------------|
| SUMMARIES | Ω | T31308 | T39116 | T40413 | A42452 | B97355 | S57810 | T24111 | S22293 | H82691 | A34203 | 854619 | H69491 | C82900 | 140758 | E90544 | D69493 | C81374 | T34536 | 875817 | T47670 | F72281 | D82163 | T43653 | D82352 | A30481 | AF3286 | D87046 | 99 | G82336 |
| | 80 | . 7 | ~ | ~ | ~ | 7 | N | ~ | | | ~ | | N | N | ~ | N | N | 74 | | | | 7 | | | • | | N | | N | N |
| | % Query Match Length | 3472 | 840 | 877 | 102 | 1498 | 225 | 425 | 670 | 749 | 2717 | 156 | 252 | | σ | 116 | 165 | 253 | 259 | 284 | 298 | 368 | 426 | 466 | 653 | 890 | 1028 | 1152 | 1394 | 1401 |
| | Query Match | 73.1 | 71.2 | 71.2 | 69.5 | 69.5 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 65.4 | 65.4 | 65.4 | 63.5 | ω. | • | 63.5 | | е. | æ. | 63.5 | 63.5 | 63.5 | 63.5 | • | 63.5 | • | ٠ | 63.5 |
| | Score | 38 | 37 | 37 | 36 | 36 | 35 | 35 | 32 | 35 | 35 | 34 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 |
| | Result No. | | 7 | m | 4 | ß | 9 | 7 | œ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 59 |

| hypothetical prote masking protein pr hypothetical prote transport protein rho protein GDP-di hypothetical prote cyclin D2 - rat cyclin D2 - rat | cyclin D2 - mouse cyclin D2 - human cyclin D2 - hrica cyclin D2 - Africa cyclin D2 - Africa cyclin D3 - zebra cyclin D3 - human cyclin D1 - tehra |
|---|---|
| T04456 A38261 B97333 PQ0616 B72481 UC4011 | A41984 A42822 S57922 JC4579 G62730 B42822 |
| 00000000 | 00000000 |
| 1548 1712 84 175 223 279 288 | 2 2 2 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 |
| 63.5 61.5 61.5 61.5 61.5 61.5 | 611.5 611.5 611.5 611.5 611.5 |
| 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 55555555555555555555555555555555555555 |
| 0 H B B B B B B B B B B B B B B B B B B | 8 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 |

ALIGNMENTS

```
hypothetical 367K protein - Cenarchaeum symbiosum
C;Species: Canarchaeum symbiosum
C;Species: Canarchaeum symbiosum
C;Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T31308
R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Peldman, R.A.; Wu, K.Y.; Swanson, R.V.
J. Bacteriol. 180, 5003-5009, 1998
R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Peldman, R.A.; Wu, K.Y.; Swanson, R.V.
A;Title: Genomic analysis reveals chromosomal variation in natural populations of the A;Reference number: 220994; MUID:98422450; PMID:9748430
A;Reference number: 220994; MUID:98422450; PMID:9748430
A;Residues preliminary; translated from GB/EMBL/DDBJ
A;Residues: L3472 csCH>
A;Residues: L3472 csCH>
A;Crose-references: EMBL:AF0833072; NID:93599393; PID:93599394; PIDN:AAC62699.1
C;Superfamily: Cenarchaeum symbiosum hypothetical 367K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 73.1%; Score 38; DB 2; Length 3472; Local Similarity 54.5%; Pred. No. 59; loss 6; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 6
```

|:|:| |:|:| 2294 EDVIPRGISFS 2304 1 BEVVPXGMSYS 11

ઠે 윱

ö

probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accesion: 19116
R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, November 1999
A;Accession: T39116
A;Accession: T39116
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-840 cHUNA
A;Residues: 1-840 cHUNA
A;Residues: BMBL:AL132779; PIDN:CAB60015.1; GSPDB:GN00066; SPDB:SPAC869.05c
A;Experimental source: Strain 972h-; cosmid c869

C;Genetics: A;Gene: SPDB:SPAC869.05c

A; Map position: 1

Gaps .. 0 71.2%; Score 37; DB 2; Length 840; 77.8%; Pred. No. 21; tive 1; Mismatches 1; Indels Best Local Similarity 77.8 Matches 7; Conservative Query Match

ö

||| ||||: 135 VVPQGMSYA 143 3 VVPXGMSYS 11

셤

ò

```
Alreiny:

Alrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zinc finger protein AT-BP2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: $2223, 178658
R;Mtcchelmore, C.; Traboni, C.; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein precursor (clone TPP11) - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cyaccession. S57810
CyAccession. S57810
CyAccession. S57810
CyAccession. S57810
CyAccession. S57810
CyAccession. S67810
CyAcce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                   ö
Score 36; DB 2; Length 1498;
Pred. No. 63;
2; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 2; Length 225;
Pred. No. 13;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.3%; Score 35; DB 2; Length 425; Best Local Similarity 50.0%; Pred. No. 26; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein R10D12.10 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 23/3; 56/3; 113/3; 257/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.3%;
          Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.3
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                           1276 BQKIPMGMSY 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 DEVVPNGKTYA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 RQIVPGGLQY 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 REVVPXGMSY 10
                                                                                                                                                                                                            1 BEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA aegregation ATPase, FtsK/SpoIIIE family, YUKA B. subtilis ortholog [imported] - Clos C; Species: Clostridium acetobutylicum
C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C; Accession: B97355
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Konin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Datesianor. A45452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
                                                                                                                                                                                                            C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40413
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
Submitted to the EMBL Data Library, August 1998
A;Reference number: 221926
A;Reference number: 221926
A;Recession: T40413
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-877 <LYN-
A;Residues: 1-877 <LYN-
A;Residues: 1-877 <LXN-
A;Resperimental source: strain 972h-; cosmid c3H7
A;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: B97355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1498 «KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: A42452
A,Molacule type: DNA
A,Residues: 1-102 <MOR>
A,Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.2%; Score 37; DB 2; Length 877; Best Local Similarity 77.8%; Pred. No. 22; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36, DB 2; Length 102;
Pred. No. 3.5;
3; Mismatches 1; Indels

    fission yeast (Schizosaccharomyces pombe)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vl protein - tobacco yellow dwarf virus (strain Australia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 69.2
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| |::||
QVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 VVPQGMSYA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Genetics:
A,Gene: CAC3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

ö

```
Nybothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
Nylternate names: hypothetical protein 02612; hypothetical protein YOL303.3
Cypecies Saccharomyces cerevisiae
C;Dete: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54619; 866879
R;Ae Haan, M.; Maarse, A.C.; Grivell, L.A.
R;Ae Haan, M.; Maarse, A.C.; Grivell, L.A.
R;Ae Hean, M.; Maarse, A.C.; Grivell, L.A.
R;Aeference number: S34617
A;Residues: 1-156 obEH>
A;Residues: 1-156 obEH>
A;Coss-references: ENBL: X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R;Ae Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66877
A;Residues: 1-156 obEN>
A;Residues: 1-150 ob
                                                                                                                                            A/Status: preliminary
A/Molecule type: mRNA

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: OS-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
C;Accession: H69491
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
     A;Title: A DNA-binding protein containing two widely separated zinc finger motifs that A;Reference number: A34203; MUID:90169514; PMID:2106471
A;Accession: A34203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.3%; Score 35; DB 2; Length 2717; 66.7%; Pred. No. 1.9e+02; ive 2; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB;
Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: hypothetical protein YOR013w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: SGD:S0005539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| |::||
2405 WPAGLTYS 2413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 BVMPLGMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               topoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: H82691
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82315; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Status: preliminary
A;Note: for a complete list of authors see reference number A59328 below
A;Status: preliminary
A;Note: for a complete list of authors see reference number A59328 below
A;Status: preliminary
A;Note: for a complete list of authors see reference number A59328 below
A;Status: preliminary
A;Note: for a complete list of authors are reference number A59328
A;Residues: l-149 csfmx
A;Residues: l-149 csfmx
A;Resperimental source: strain 9a5c
B;Simpor, A.J.G; Reinard, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S; Bueno, M.R.P.; Camargo, A.B.; Ferreira, A.J.S.
Briones, M.R.S; Bueno, M.R.P.; Camargo, A.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.S.; Kuramae, B.S.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, E.M.; Miyaki, C.Y.; Anathors: Martins, B.M.F.; Mateukuma, A.Y.; Martins, R.B.; Mateukuma, A.Y.; Martins, R.B.; Mateukuma, A.Y.; Martins, R.B.; Mateukuma, A.Y.; Martins, R.M.; Silva, A.G. & Sa, A.J. de Sa, A.J. de Sa, R.G.; Santelli, W.; P. A; Verence number: A59228
A;Reference number: A59228
A;Reference number: A59228
A;Cortester
A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-Kefezenece number: IS8280; MUID:91187610; PMID:1901405
A;Accession: 822293
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: XP1353
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding protein PRDII-BPI - human N;Alternate names: major histocompatibility complex enhancer-binding protein 1 C;Species: Homo sapiens (man) C;Date: 22-Jum-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999 C;Accession: A34203; A34779 R;Fan, C.M.; Maniatis, T. Genes Dev. 4, 29-42, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                           A Molecule type: mRNA
A;Residues: 1-670 <MIT>
A;Residues: 1-670 <MIT>
A;Cross-references: RMBL:X54250; NID:g57519; PIDN:CAA38151.1; PID:g57520
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35, DB 2; Length 670;
Pred. No. 43;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 2;
Pred. No. 48;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.3%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 VVPAGLTYS 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVDPSGMSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

Gaps

ö

ö

Gaps

ö

2; Indels

```
508 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C,Species: Mycoplasma pulmonis
C,Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C,Aacession: E90544
R;Chambaud, 1.; Heilig, R.; Perris, S.; Barbe, V.; Samson, D.; Galisson, P.; Moszer, I
N,Claic Acids Res. 29, 2145-2153, 2001
A,Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pu
A,Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                        A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            윱
                  A Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaect A; Prite: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaect A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-252 cKLE>
A; Residues: 1-252 cKLE>
A; Cross-references: GB: AE000970; GB: AE000782; NID:92689293; PIDN: AAB89318.1; PID:9264866
C; Superfamily: cell division inhibitor minD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein 1 - Campylobacter jejuni (fragment)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Date: 140758; 847317
R;Hani, B.K.; Chan, V.L.
J. Bacteriol. 177, 2396-2402, 1995
A;Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd A;Reference number: 140758; MUID:95247673; PMID:7730270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum C.Species: Ureaplasma urealyticum C.Species: Ureaplasma urealyticum C.Species: Ureaplasma urealyticum C.Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C.Accession: C82900 R.Species: 18-Aug-2000 R.Species: 18-Aug-2000 R.Species: 18-Aug-2000 R.Species: 0.1:; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H. Bubmitted to GenBank, Pebruary 2000 A.Speciption: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A.Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-544 <GLA>
A;Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-94 <RES>
A; Cross-references: RMBL: Z36940; NID: g535805; PIDN: CAA85392.1; PID: g535806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 544;
55;
                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2; Length 252;
Pred. No. 24;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 2; Length 94;
Pred. No. 14;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%;
55.6%;
                                                                                                                                                                                                                                                                                                                                             65.4%;
ilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 REVVPHYLSY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: | ||||
26 DIFPSGMSY 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:| |||
81 EVIPAGMS 88
Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVVPXGMS 9
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: G;Genetics: A;Gene: ABCsbp-5; UU359 A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: C82900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

```
ö
A;Molecule type: DNA
A;Residues: 1-116 «KUR»
A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                      Score 33; DB 2; Length 116;
Pred. No. 17;
0; Mismatches 2; Indels
                                                                                                             AjGana: MYPU 2610
AjGanatic code: SGC3
CjSuperfamily: Bscherichia coli ribosomal protein L20
                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: December 22, 2003, 17:44:57 Job time : 9.06667 secs
                                                                                                                                                                                                        Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                   3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                68 VRPLGMSYS 76
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

December 22, 2003, 16:43:51; Search time 4.6 Seconds Run on:

(without alignments) 112.455 Million cell updates/sec

US-09-909-164-10 52 1 BEVVPXGMSYS 11 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

| | | Description | Q8rg86 fusobacteri | 074377 schizosacch | | Q04351 clostridium | P15822 homo sapien | | | _ | | P45489 campylobact | Q9d387 mus musculu | Q9krb0 vibrio chol | | Q9nzm5 homo sapien | | _ | | | Q14766 homo sapien | | Q8cg19 mus musculu | | | _ | | xenopn | | xenopu | | 1 homo | 5 homo | 5322 mus r | D200AD TETTION DAY |
|-----------|--------|-----------------|--------------------|--------------------|------------|--------------------|--------------------|------------|------------|------------|------------|--------------------|--------------------|--------------------|------------|--------------------|------------|------------|------------|------------|--------------------|----------|--------------------|----------|------------|------------|------------|------------|------------|--------|------------|------------|------------|------------|--------------------|
| SUMMARIES | | QI | CARB FUSIN | SULH SCHPO | Y11K TYDVA | Y1A9_CLOAB | ZEP1 HUMAN | CY14 NEUCR | A10C HUMAN | RL20 MYCPU | YJ49 ARCFU | Y990 CAMJE | CTX3 MOUSE | AROA_VIBCH | CC37_SCHPO | GSR2 HUMAN | BCNS_CLOPE | LTBS_MOUSE | LTBS HUMAN | RPOC_VIBCH | LTBL HUMAN | LTB1_RAT | LTBL_MOUSE | CGD2_RAT | CGD2_HUMAN | CGD2_MOUSE | CGD1_BRARE | CGD1_XENLA | CGD2_CHICK | | CGD1_CHICK | CGD3_HUMAN | CGD1 HUMAN | CGD1_MOUSE | ביים "ניניט |
| | | Match Length DB | 1058 1 | | 102 1 | 1498 1 | | 788 | 1499 | | | 253 1 | 280 1 | | 466 1 | | | | | 1401 1 | | | | | | | | | | | | 292 1 | 295 1 | 295 1 | |
| , | ouery | | | 7 71 | 69 9 | 36 69.2 | 5 67 | | 9 | | е | 13 63.5 | 3 63. | 3 63. | 13 63.5 | 3 63. | 63. | | 63. | | 63. | 63 | 63. | 61. | 32 61.5 | 61. | 61. | 61. | 61. | 61. | 61. | 32 61.5 | 61. | 61. | 5 |
| | Result | No. Score | 1 3 | 7 | е С | 4. | S. | 9 | 7 3 | 9 | 6 | 10 3 | | 12 3 | | 14 3 | 15 3 | 16 3 | 17 3 | 18 3 | 19 3 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 3 | |

| P44677 haemophilus 075355 homo sapien | 29y616 homo sapien P90518 crithidia f | 732394 numan nerpe 732784 saccharomyc 762671 rattus norv | P28931 tomato aspe P16916 escherichia P16918 escherichia | P16917 escherichia 095071 homo sapien |
|--|--|--|--|--|
| P O | ORI | чио | р д д | 1 th O |
| | | | | |
| TOLB HABIN ENP3 HUMAN | S216 HUMAN GSP CRIPA | SCT1_YEAST EDD FAT | V1A_TAV RHSA_ECOLI RHSC_ECOLI | RHSB_RCOLI EDD_HUMAN |
| | | ٠, | | יהה |
| 427 529 | 691 719 | 759 920 | 993 1377 1397 | 1411 |
| 61.5 | 61.5 | 61.5 | 61.5 | 61.5 |
| 32 | 355 | 3 2 2 | 2 2 2 2 | 333 |
| 3.4 3.5 | 37 | 8 6 8 0 | 444 424 | 44 |

ALIGNMENTS

```
MEDINE-2186534; PubMed=11889109;

Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Battacharrya A., Battman A., Gardner W., Garchkin G., Zhu L.,

Ray Vasieva O., Chu L., Kogan Y., Chaper W., Galtsman E., Bernal A.,

Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

Ray Tomore and analysis of the oral bacterium Fusobacterium

RT nucleatum strain ATCC 25586. "

J. Bacteriol. 184:2005-2018(2002)

I. Garchylty C. Arp + L-glutamine + CO(2) + H(2)O = 2 ADP +

phosphate + L-glutamate + carbamoyl phosphate.

C. -I COPACTOR: Binds 3 manganese ions per subunit (By similarity).

C. -I PATHWAY: Arginine biosynthesis.

C. -I PATHWAY: Pyrimidine biosynthesis, first step.

C. -I SUBBNIT: Composed of two chains, the small (or glutamine) chain

promotes the hydrolysis of glutamine to ammonia, which is used by

the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).

C. -I SIMILARITY: BELONGS TO THE CARB PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp.ch).
                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
                                                                                                                                                                                           CARBOR FN0422.
Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                          PRT; 1058 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE010554; AAL94625.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_01210; -; 1.
InterPro; IPR006275; CarA L_glu.
InterPro; IPR005483; CPase_L.
InterPro; IPR005480; CPase_L.D2.
InterPro; IPR005480; CPase_L.D3.
InterPro; IPR005481; CPase_L.N.
InterPro; IPR004362; MGS_IIKe.
Pfam; PF00289; CPSase_L.Chain; 2.
Pfam; PF00289; CPSase_L.D2; 2.
Pfam; PF02786; CPSase_L.D3; 1.
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 25586;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=76856;
                                                                                                                                                                                                                                                           Pusobacterium
                                          CARB FUSIN
                      CARB FUSIN
RESULT 1
```

```
-1- FUNCTION: HIGH APPINITY UPTAKE OF SULPATE INTO THE CELL (BY SIMILARITY).
                  genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYDVA
                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A REPORT OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLIANS-2184401; PubMed=11859360;
WEDLIANS-21840401; PubMed=11859360;
WEDLIANS-21840401; PubMed=11859360;
WODG V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squores U., Beronn S., Chillingworth T., Churcher C.M.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
A collins M., Connor R., Cronin N., Harris D., Hidalgo U., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huch E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
A Huherford K., Rutter S., Sauders R., Stevens K.,
A Rutherford K., Taylor R.G., Tivey A., Walbh S.V., Warren T., Whitehead S.,
A Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A Taylor K., Taylor R.G., Tivey A., Walbh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Gablbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
A Dominguez A., Revuelta J.L., Moreno S., Annestrong J., Forsburg S.L.,
A Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
R PIGREAMS, TIGRIAGS, CPSASE.
R TIGREAMS, TIGRI369, CPSASE.
R PROSITE; PRO0098; CPSASE.
R PROSITE; PS00866; CPSASE.
R PROSITE; PS00867; CPSASE.
R PROSITE; PS00867; CPSASE.
R Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
KW Arginine biosynthesis; Complete proteome.
CARBOXPHOSPHATE SYNTHETIC DOMAIN.
FT DOMAIN 402 546 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
FT DOMAIN.
FT ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

117451 MW; ED7037AF77CIE39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; Length 1058;
Pred. No. 6.3;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           877 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable sulfate permease C3H7.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|| |::||
190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                               153
302
2384
300
832
832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULH SCHPO
074377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPBC3H7.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                  REPEAT
REPEAT
NP BIND
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
SULH_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MODITINE 32188538, Pubmed=1546458,

MOTIS B -A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

Morris B -A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component of

"The nucleotide sequence of the infectious cloned DNA component of

"The nucleotide sequence of the infections of geniniviruses

infecting monocotyledonus plants.";

Virology 187:613-642(1992).
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
-i- SIMILARITY: Contains 1 STAS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.2%; Score 37; DB 1; Length 877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 747 SIAS.
877 AA; 96373 MW; 56995A8493371B43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; 8sDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y11K_TYDVA STANDARD; PRT; 102 AA. P31619; 01-JUL-1993 (Rel. 26, Created) 01-GWL-1993 (Rel. 26, Last sequence update) 01-OCT-1993 (Rel. 27, Last annotation update) Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                               Geneba Sponde, SPEC3H7.02; -.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulph_transpt.
Pfam; PP001140; STAS; 1.
Pfam; PP00916; Sulfate_transp; 1.
TIGRPAM6; TTGR00815; BILP; 1.
PROSITE; PS010130; SLC26A; 1.
                                                                                                                                                                                                                                                                                                                                            EMBL; AL031261; CAA20298.1; -. PIR; T40413; T40413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77...
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 VVPQGMSYA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; seDNA vi:
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport;
TRANSMEM
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license4seb.sib.ch).
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a small heat shock protein of Clostridium acetobutylicum.";
U. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: Contains 2 PtsK/SpoIIIE domains.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MBDLINB=21359325; PubMed=11466286;
Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin R.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium acetobutylicum.
Bacteria; Pirmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                   Score 36; DB 1; Length 102;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                    102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 28, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1498 AA.
                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; PubMed=8501044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X65276; CAA46379 1; ALT_FRAME.
PIR; B97355; B97355.
InterPro; IPRO2543; Ft&K SpOIIE.
Pfam; PF01580; Ft&K_SpOIIE; 2.
                                                                                                                                                                       PIR; A42452, A42452.
InterPro; IPR002631; Gemini mov.
Pfam; PP01708; Gemini_mov; T.
Hypothetical procein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE007866; AAK81629.1; -.
                                                                                                                                                                                                                                                                                       69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein CAC3709.
                                                                                                                                                     EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        OVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                  2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y1A9_CLOAB
ID _Y1A9_CLOAB
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204351;
 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-BP) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Blochemistry 31:3907-3917(1992).

-1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SY40, CMY, OR HIV1. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MHC, INTERLEUKIN-2 RECEPTOR, AND INTERPERON-BETA GENES. IT MAY ACT
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Blochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN T-CELL ACTIVATION.
SUBCELLULAR LOCATION: Nuclear.
INDUCTION: BY MITOGEN AND PHORBOL ESTER.
DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan C.M., Maniatis T.;
"A DNA-binding protein containing two widely separated zinc finger
motifs that recognize the same DNA sequence.";
Genes Dev. 4:29-42(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa; Chordata; Crantata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NWR OF 2087-2142.
MEDLINE-92232684; PubMed-1567844;
Cmichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E. Gronenborn A.M.;
                                                                                                                                                                            ö
PROSITE; PS50901; FTSK_SPOIIIE; 2.
Hypochetical protein; ĀTP-binding; Complete proteome; Repeat.
DOMAIN 655 857 FTSK/SPOIIE 1.
NP BIND 675 682 ATP (POTENTIAL).
                                                                                                                                  Score 36; DB 1; Length 1498;
Pred. No. 24;
2; Mismatches 2; Indels
                                                                                             1498 AA; 168968 MW; FF42037A335A9649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 2113-2142.
MEDLINE-91064333; PubMed-2248949;
Omlchinski J.G., Clore G.M., Appella B., Sakaguchi K.,
                                                                                                                                                                                                                                                                                                                                                  2717 AA.
                                                                           FTSK/SPOILIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC-FINGER IN-BETWEEN. SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=90169514; PubMed=2106471;
                                                                                                                                69.2%;
60.0%;
                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                   |::| ||||
1276 BQKIPMGMSY 1285
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                             1188
                                                                                                                                                                                                              1 EBVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIVBPI OR ZNP40.
                                                                                                                                                                                                                                                                                                                                            ZEP1 HUMAN
P15822,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PRDII-BF1)
                                                     NP BIND
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                               ZEP1_HUMAN
   8311138
                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                        "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EC 3.6.3.1) (ATPVC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21313119; PubMed=11353404;
Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ATPase gene ATP10C maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21225279; Pubmed=11326269;
Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh
Oshimura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 788;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LINKED (GLCNAC. . .) (PC 4FC604B60798CE77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A10C HUMAN STANDARD; PRT; 1499 AA. 060312; 096914; 39. MAY-2000 (Rel. 39, Created) 28-PEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Potential phospholipid-transporting ArPase VC Aminophospholipid translocase VC; ATPIOC OR ATPVC OR KIAAOS66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 32;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                          Transport, Transmembrane, Glycoprotein.
TRANSMEM 71 91 POTENTIAL.
TRANSMEM 103 123 POTENTIAL.
                                                                                                                                                                                                                                                                                                   EMBL, MS9167, AAA33615.1, ALT_SEQ.
InterPro; IPR001902; Sulph_transpt.
                                                                                                                                                                                                                                                                                                                                    Pfam; PP00916; Sulfate transp; 1.
TIGRFAMB; TIGR00815; Bulp; 1.
PROSITE; PS01130; SLC26A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87864 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494
23
578
                                                                                                                                                                                                                                                                                                                                                                                                                                                148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213
291
346
383
471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 VVPQGMAYA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363
451
474
23
578
788 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A10C HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                      DR GO; GO:0005537; F:DNA binding activity; TAS.

DR GO; GO:0005677; F:DNA binding activity; TAS.

DR DR GO; GO:0005677; F:DNA binding activity; TAS.

DR Fiam; PR001067; Zif C212.

DR PROSITE; PS000028; ZINC FINGER C212.

DR PROSITE; PS00028; ZINC FINGER C212.

DR PROSITE; PS50157; ZINC FINGER C212.

DR PROSITE; PS50167; ZINC FINGER C212.

DR PROSITE PS50167; ZINC FINGER C212.

DR PROSITE PS50167; ZINC F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94188926; PubMed=8140616;
Sandal N.N., MarcKer K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
permease II and a putative human tumour suppressor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and DNA recognition
lfate permease II in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
Ketter J.S., Jarai G., Ru Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recogn elements of cys-H, the structural gene for sulfate permease Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 1; Length 2717;
Pred. No. 73;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297217 MW; D45D3CA951FEA561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         C2H2-TYPE.
C2HC-TYPE (POTENTIAL).
C2H2-TYPE.
C2H2-TYPE.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sulfate permease II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         788 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 30:1780-1787(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.3%;
                                                                                                        PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
TRANGFAC; 700497; -.
Genew; HGNC:4920; HIVEP1.
                                                                         EMBL; X51435; CAA35798.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| |::||
2405 VVPAGLTYS 2413
                                                                                                                                                                                                                                                                                                                                                                                                                981
2109
2139
806
2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2109
2116
2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2095 209
2099 210
2109 210
2115 211
2123 212
2127 213
                                                                                           PIR; A34203; A34203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         ZN_FING
ZN_FING
ZN_FING
DOMAIN
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P23622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CY14 NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGRN
   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

Gaps

ö

. S

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISEASE: Defects in ATP10C are a cause of Angelman syndrome (AS) [MIM:105830]; also known as 'happy puppet syndrome'. It is characterized by features of severe motor and intellectual retardation, microcephaly, ataxia, frequent jerky limb movements and flapping of the arms and hands, hypotonia, hyperactivity, hypotymentation, seizures, absence of speech, frequent smiling and episodes of paroxysmal laughter, and an unusual facies characterized by macrostonia, a large mandible and open-mouthed expression, a great propensity for protruding the tongue ('tongue thrusting'), and an occipital groove.

SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
                                                                                                                                                                                    Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomta N., Ohara O.;
Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 5:31-39(198).
-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
-!- CATALYTIC ACTIVITY: Mide expression, with highest levels in
kidney, followed by lung, brain, prostate, testis, ovary, and
small intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO: 00.0016021; C:integral to membrane; NAS.
GO: 00.0016021; F:phospholipid-translocating ATPase activity; NAS.
GO: GO:0008160; P:regulation of cell shape; NAS.
InterPro: IPR001757; ATPase E. I. E. InterPro: IPR00539; Flippase.
InterPro: IPR00539; Flippase.
InterPro: IPR00539; Hydrolase.
Pfam; PF007702; Hydrolase; I.
PRINTS; PR00119; CATATPASE.
IGRPAMs; TIGR01652; ATPase-Plipid; I.
IGRPAMs; TIGR01652; ATPase-Plipid; I.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
adjacent to UBE3A and exhibits similar imprinted expression."; Am. J. Hum. Genet. 68:1501-1505(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB051358; BAB47392.1; --
EMBL; AY029564; AAX33100.1; --
BMBL; AY02948; AAX33100.1; JOINED.
EMBL; AY029489; AAX33100.1; JOINED.
EMBL; AY029489; AAX33100.1; JOINED.
EMBL; AY029499; AAX33100.1; JOINED.
EMBL; AY029491; AAX33100.1; JOINED.
EMBL; AY029492; AAX33100.1; JOINED.
EMBL; AY029495; AAX33100.1; JOINED.
EMBL; AY029496; AAX33100.1; JOINED.
EMBL; AY029496; AAX33100.1; JOINED.
EMBL; AY029496; AAX33100.1; JOINED.
EMBL; AY029499; AAX33100.1; JOINED.
EMBL; AY029499; AAX33100.1; JOINED.
EMBL; AY029499; AAX33100.1; JOINED.
EMBL; AY029499; AAX33100.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED
                                                                                                                           TISSUE=Brain;
MEDLINE=98290545; PubMed=9628581;
                                                            [3]
SEQUENCE OF 337-1499 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMEL; AY029491; AAX33100.1; OREMEL; AY029494; AAX33100.1; OREMEL; AY029494; AAX33100.1; OREMEL; AY029496; AAX33100.1; OREMEL; AY029499; AAX33100.1; OREMEL; AY029499; AAX33100.1; OREMEL; AY029499; AAX33100.1; OREMEL; AY029500; AAX33100.1; OREMEL; AY029502; AAX33100.1; OREMEL; AY029503; OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
```

Of CHAC BUDUILL (BY BIMILIAILLY).
-1- SIMILARITY: BELONGS TO THE L20P PAMILY OF RIBOSOMAL PROTEINS. 38888888888

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).

Gaps

ö

Indela

.. ..

1; Mismatches Pred. No. 10;

60.04;

```
6; Conservative
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                           Y990 CAMJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                셤
                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-VC-16 / DSW 4304 / ATCC 49558;

MEDLINE-98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.B.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Fleischmann R.D., Quackenbush A., McKenney K., Adams M.D., Loftus B.,

Fleischmann R.D., Dungherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%; Score 33; DB 1; Length 165;
                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 33; DB 1; Length 116; 77.8%; Pred. No. 7.1; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 7 27 20 POTENTIAL
                                                                                                                                                                                                                                                                                           g; Complete proteome.
C59C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaeoa; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BBC17054810ADBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 41, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                    EMBL; AL445563; CAC13434.1; -. PIR; B90544.
Mypulist; MYPU 2610; -. HAWAP, MF 00382; -; 1.
InterPro; IPR005813; L20.
InterPro; IPR005813; L20.
InterPro; IPR005812; L20.bact_org.
Pfam; PF00453; Ribosomal_L20; 1.
PRINTS; PR00062; RIBOSOMĀLL20.
ProDom; PD002389; L20; 1.
TIGRRĀMS; TIGR01032; rplT bact; 1.
RNOSITE; PS00937; RIBOSOMĀL L20; 1.
Ribosomal proteān; FRNA-bināing; Comg SEQUENCE 116 AA; 13565 MW; C59C74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000968; AAB89307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17588 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein AF1949.
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 VRPLGMSYS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; D69493; D69493.
TIGR; AF1949; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YJ49 ARCFU
028330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YJ49_ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SY WE DER DER DER SY WE SEND WE SY WE SY WE SY WE SEND WE SY WE SY WE SY WE SY WE SY WE SEND WE SY WE SY WE SY WE SEND WE SEND WE SY WE SEND WE SEND W
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its way muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=NCTC [1168;
MEDLINE=20150912; PubMed=10688204;
MEDLINE=20150912; PubMed=10688204;
MEDLINE=20150912; PubMed=10688204;
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jasham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jasham D., Chillingworth T., Davies R.M., Peltwell T., Holroyd S., Jasham D., Chillingworth T., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
VCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 160-253 FROM N.A.
STRAIN=ATCC 43431 / TGH 9011;
MEDLINE=55247673; PubMed=7730270;
Hani B.K., Chan V.L.;
"Expression and characterization of Campylobacter jejuni benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 253;
Pred. No. 16;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; C81374; C81374.
PIR; 140758; 140758.
Hypotherical protein; Complete proteome.
SEQUENCE 253 AA; 29783 MW; P96D3FP3265F8A6A CRC64;
                                                                                                                                                                                                                                P45489; Q9PNVO;
01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTX3_MOUSE STANDARD; PRT; 280 AA Q9D387; Q9CXQ4; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update)
                                                                                                                                                                                                           253 AA
                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 177:2396-2402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL139076; CAB73246.1; -.
                                                                                                                                                                                                                                                                                                                                      Hypothetical protein Cj0990c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z36940; CAA85392.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                              STANDARD;
                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: | ||||
185 DIPPSGMSY 193
1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EVVPXGMSY 10
                                       60 EESIPDGASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4484
```

```
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

STRAIN=C57BL/6J; TISSUE=Embryonic head;
MEDLINE=21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arawawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S.,
Arawawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov G., Quackenbush J.,
Rochim D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Baka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Wanabhizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RP SEQUENCE FROM N.A. (ISOPORM 2).

RC TISSUE-Amammary fibroblast:

RA STEAUBDETS, PubMed-12477932;

RA STRAUBDETS R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Heiber F.,

RA Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Heiber F.,

RA Billechul S. Borates M.B., Bonaldo M.F., Carainci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McWan P.J., McKernan K.J., Malek J.A., Guaraten P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Nilialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Radan A., Young A.C., Scheutz J., Myers R.M.,

RA Hutting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length
                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLUIAR LOCATION: Type I membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
15-SEP-2003 (Rel. 42, Last annotation update) Protein C20orf103 homolog precursor. C20ORF103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9D387-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.";
                                                                    Mus musculus (Mouse)
                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1
```

Gapa

ö

2; Indels

Pred. No. 18; 0; Mismatches

63.5%;

Query Match Best Local Similarity 75.0-

CONFLICT CONFLICT SEQUENCE

셤 ò

Score 33; DB 1; Length 280;

(POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL)

PROTEIN C200RP103 HOMOLOG. EXTRACELLULAR (POTENTIAL).

Fransmembrane; Signal; Alternative splicing.

EMBL; AKO1822; BAB31124.1; ALT_FRAME. EMBL; BCO47731; AALD4791.1; -... MGD; MGI:1920368; 3110035N03Rik. MGD; MGI:1923411; 6330527006Rik.

CYTOPLASMIC (POTENTIAL)

30 236 257 35 102 127

CARBOHYD CARBOHYD CARBOHYD VARSPLIC CONPLICT

DOMAIN TRANSMEM DOMAIN

STREETFFFFFFFFFFFFFFFFF

SIGNAL

POTENTIAL.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as 100g as 1ts content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=BI TOR Ni5961 / Serctype Ol;

MEDLINE=204060313; PubMed=10952301;

Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Endless S., Nelson K.B., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Pleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 406:477-483(2000).
-!- CATALTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate = -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase)
AROA OR VC1732.
                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBUNIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: Belongs to the EPSP synthase family.
                                              426 AA.
                                                                                       28-PBB-2003 (Rel. 41, Created)
                                           STANDARD;
                                                                                                                                                                                                                                  Vibrio cholerae
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholerae.";
                                         VIBCH
                                                               Q9KRB0;
              AROA VIBCH
RESULT 12
```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch). Isold=Q9D387-2; Sequence=VSP 003820; CAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 174 and 239.

```
region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLTSCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSR2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECOURDING FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RA MEDINE=218401; PubMed=11859360;

RA MEDINE=218401; Path N., Hayles J., Baker S., Basham D., Bowman S.,

RA WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA HOLFOYd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,

RA HOLFOYD S., Hornsby T., Howarth S., McDonald S., McLean J.,

RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Money P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,

RA Money P., Simmonds M., Saunders D., Quail M.A., Rabbinowitsch B.,

Rutherford K., Rutter S., Saunders D., Quail M.A., Rabbinowitsch B.,

Rutherford K., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Woodward J., Volckaert G., Aert R., Robben J., GTymonprez B.,

Woodward J., Volckaert E., Rieger M., Schaefer M., Mueller-Auer S.,

Rabel C., Puchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Goffeau A., Cadieu E., Diamermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Diamer S., Gloux S., Lelaure V., Mottler S.,

RA Goffeau A., Cadieu E., Diamerz S., Hunt C., Moore K., Hurst S.,

RA Lucas M., Rochet M., Gallardin C., Mole Rey F., Benito J.,

RA Dagar R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dagar R.R., Cruzado L., Jimenez S., Armstrong J., Forsburg S.L.,

RA Dagar R.R., Cruzado L., Jimenez S., Armstrong J., Forsburg S.L.,

RA Dagar R.R., Revuelle J., Moreno S., Armstrong J., Forsburg S.L.,

RA Daninguez A., Revuelle J., Moreno S., Almstrong J., Forsburg S.L.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HSp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
                                                                                                                                                 TIGRFAMS; TIGR01356; aroA; 1.
PROSITE; PS00104; BPSP SYNTHASE 1; 1.
PROSITE; PS00865; BPSP_SYNTHASE 2; 1.
Aromatic amino acid losgynthesis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                              1; Length 426;
                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Westwood D.K.; Fantes P.A.; Westwood P.K.; Preston N.C.; Fantes P.A.; "Schizosaccharcomyces pombe cdc37 gene."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetacese;
                                                                                                                                                                                                                                                                                                                                                                                                                    466 AA.
                                                                                                                                                                                                                                            Score 33; DB
Pred. No. 28;
                                                                                                                                                                                                                                                                           1; Mismatches
email to license@isb-sib.ch).
                                                                      HAMAP; MF_00210; -; 1.
InterPro; IRR006264; AroA.
InterPro; IPR001986; BFSP_syntase.
Pfam; PF00275; BPSP_synthase; 1.
ProDom; PD001867; EPSP_syntase; 1.
                            EMBL; AE004251; AAF94882.1; -. PIR; D82163; D82163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                            63.5%;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                         223 EFVIPAGQSY 232
                                                                                                                                                                                                                                                                                                         1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
NCBI_TaxID=4896;
or send an
                                                                                                                                                                                                                                                                                                                                                                                                                    SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                               094740:
                                                                                                                                                                                                                                                                                                                                                                                                      CC37_SCHPO
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22988257; PubMed=12477932; Straubberg R.L., Peingold B.A., Grouse L.H., Derge J.G., Straubberg R.L., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Browmetein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Browmetein M.J., McGerlas G.J., Abramenon R.D., Mullahy S.J., Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE-20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glloma tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                                                ö
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSR2_HUMAN STANDARD; PRT; 478 AA.
Q9NZM5; Q9BTC6; Q9HX6; Q9NPP1; Q9NPR4; Q9UF12;
16-OCT-2001 [Rel. 40, Created]
16-OCT-2001 [Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%; Score 33; DB 1; Length 466; 50.0%; Pred. No. 30; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GeneDB SPombe; SPBC9B6.10; -.
InterPro; IPR004918; Cdc37.
Pfam; PF03234; Cdc37; Cc27; Cc27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ132377; CAB38758.1; -. EMBL; AJ132376; CAB38757.1; -. EMBL; AL049769; CAB42371.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 64:44-50(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 REVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; T43653; T43653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Muscle;
```

```
Best Local Similarity
                    Query Match
                                                                          ઠે
                                                                                                  셤
                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBGNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
-1- SIMILARITY: BELONGS TO THE GLTSCR2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTIG=VAR 011486.

0625 -> HG (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

RRKEQLWEKLAKÇGELPREVRRAQARLLAVPSATRAKDGPQD

TYUERP -> SGRSSYCRSWPSRASSPCGAQGPSPVAQPFCN

KGPNAPGHRIAA (IN REF. 3).

SDNPLDRPLVGQDEFFIE -> LNNPDKPVVWPGCLFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A -> S (IN REF. 2, AAH04229).
D -> H (IN REF. 3).
DEGNILLEDRYESFQRRNMIEPRERAKFKKYKVKLVEKRAF.
REIQ -> VLTVSCRGAPCPVMTPSLLPVPFRGYGRHHGCP.
WAGFVGPMPRG (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGNILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRFR
EIQL -> RGQHSFETGSRAFRGGI (IN REF. 3).
7F18923E348CB52B CRC64;
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                       [3]
SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
SEQUENCE 99-478 FROM N.A., AND SUBCELLULAR LOCATION.
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus I regulatory proteins ICP22 and ICP0 is modified in a cell-type specific manner and is recruited to the nucleus after infection.";
                                                                                                                                                                                                                                                                                                                                                                 Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              SEQUENCE OF 12-478 FROM N.A.
Andreu N., Bativill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0008181; F:tumor suppressor; TAS. Nuclear protein; Polymorphism.
VARIANT 389 389 R -> Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC006311; AAH06311.1; --
EMBL; AF296124; AAH10095.1; --
EMBL; AL359315; CAB94786.1; --
EMBL; AL359315; CAB94786.1; --
EMBL; AL359315; CAB94781.1; --
EMBL; AL125063; CAB94781.1; --
EMBL; AL122063; CAB94781.1; --
SWISS-2DPAGE; Q9NZMS; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF182076; AAF62873.1; -. EMBL; BC004229; AAH04229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 AA; 54417 MW;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 218-477 FROM N.A. TISSUE=Testis;
                                                                                                                                                                                                                                                    J. Virol. 73:3810-3817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:4333; GLTSCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235
417
477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
417
433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
                                                     ö
                                                  Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garnier T., Cole S.T.; Studies of UV-inducible promoters from Clostridium perfringens in vivo and in viron ", Mol. Microbiol. 2:607-614(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garnier T., Cole S.T.;
Complete nucleotide sequence and genetic organization of the
Dacteriorinogenic plasmid, pIP404, from Clostridium perfringens.";
Plasmid 19:134-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garnier I., Cole S.T.; "Characterization of a bacteriocinogenic plasmid from Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1; Length 890;
Pred. No. 60;
Score 33; DB 1; Length 478;
Pred. No. 31;
                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 HYDROPHOBIC.
96699 MW; F4E5E8971C31C6C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         perfringens and molecular genetic analysis of the bacterlocin-encoding gene."; J. Bacteriol. 168:1189-1196(1986).
                                                                                                                                                                                                                                                                                                                 (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                      890 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ol. Microbiol. 2:607-614(1988).
                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A30481; A30481.
InterPro; IPR003646; SH3 bac.
InterPro; IPR00084; Zn_carbopept.
Pfam; PF00246; Zn_carbopept; 1.
SWART; SM00287; SH3b; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88336297; Pubmed=2901768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89039249; PubMed=2460717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- INDUCTION: By UV irradiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87057020; PubMed=2877971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibiotic; Bacteriocin; Plasmid.
63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M14481; AAA98248.1; -. EMBL; M32882; AAA98249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA98249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-14 FROM N.A. STRAIN=CPN50;
                                               6; Conservative
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium perfringens.
                                                                                                                                          239 EVAPAGASYN 248
                                                                                               2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           890 AA;
                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Bacteriocin BCN5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CPN50;
                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (
01-JAN-1988 (
01-OCT-1994 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CPN50;
                                                                                                                                                                                                                    RESULT 15
BCNS_CLOPE
ID BCNS_CLOPE
AC P08696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

0; Gaps 2; Indels 1; Mismatches Search completed: December 22, 2003, 17:42:26 Job time : 4.6 sec8 6; Conservative 2 EVVPXGMSY 10 |||| | :| 170 EVVPGGFTY 178 Matches ઠે g

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

December 22, 2003, 17:27:26; Search time 25.2 Seconds (without alignments) 112.642 Million cell updates/sec Run on:

US-09-909-164-10 52 1 REVVPXGMSYS 11 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 23:* Датараве :

sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp archea:*
sp_bacteria:*
sp_fung1:*
sp_fung1:*
sp_human:*
sp_nammal:*
sp_mammal:*
sp_organe1e:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_rodent:*
sp_vitus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | O8dihO synechococc | O98fxl rhizobium l | O74056 cenarchaeum | Q9ury8 schizosacch | Q8ewd4 mycoplasma | Q8r126 mus musculu | Q8vd18 mus musculu | Q8btx4 mus musculu | Q8bk35 mus musculu | Q40129 lycopersico | O9xvk4 caenorhabdi | Q8c1d7 mus musculu | 043733 homo sapien | Q9bh83 plasmodium | O9bha5 plasmodium | Q81587 plasmodium |
|----|--------------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|
| | ID | 08DIH0 | 098FX1 | 074056 | Q9URY8 | Q8EWD4 | Q8R126 | Q8VD18 | Q8BTX4 | Q8BK35 | 040129 | Q9XVK4 | Q8C1D7 | 043733 | 09внв3 | Q9BHA5 | Q815S7 |
| | B | 16 | 16 | н | m | 16 | 11 | 1 | 11 | 11 | 10 | Ś | 1 | 4 | ß | 'n | S |
| | Query Match Length DB | 1044 | 387 | 3472 | 840 | 1123 | 471 | 484 | 484 | 484 | 225 | 425 | 495 | 556 | 583 | 583 | 583 |
| de | Query Match | 75.0 | 73.1 | 73.1 | 71.2 | 71.2 | 69.2 | 69.2 | 69.2 | 69.2 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 |
| | Score | 39 | 38 | 38 | 37 | 37 | 36 | 36 | 36 | 36 | 35 | 35 | 35 | 35 | 35 | 35 | 35 |
| | Result No. | 1 | 7 | 3 | 4 | ស | 9 | 7 | œ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |

| 001487 rattus ratt Q8pmi6 xanthomonas Q8pat2 xanthomonas Q9pdm6 xy1ella fas | U14122 nomo sapien Q12479 saccharomyc Q97182 sulfobus Q28342 archaeoglob Q96mul homo sapien | Q92md6 rhizobium m Q84ym3 homo sapien Q98bp5 rhizobium l Q9pqd2 ureaplasma Q9urr4 penicillium | Q89415 bifidobacte Q8xt05 ralstonia s Q8xx62 methanopyru Q8ypp5 xanthomonas Q8vus8 lactococcus Q8ktq4 candidatus | QBress fusobacter1 P74187 synechocyst Q9m3C0 arabidopsis Q9qce7 soil-borne Q9q9q7 soil-borne Q9q9q8 soil-borne Q9q9q9 soil-borne Q9q9q9 soil-borne Q9q9q5 soil-borne |
|--|---|---|---|--|
| 11 Q01487 16 Q8PMI6 16 Q8PAT2 16 Q9PDM6 | 4 U14124 3 Q12479 17 Q971S2 17 Q28342 4 Q96MU1 | 16 Q92MD6 4 Q8IYM3 16 Q98BP5 16 Q9PQD2 3 Q9URR4 | 16 Q8G415 16 Q8XT05 17 Q8XX62 16 Q8PPP5 2 Q8VUA8 2 Q8KTQ4 | 16 QRRE56 116 P74187 12 Q9QCR7 12 Q9QCR7 12 Q9DJG4 12 Q9DJ91 12 Q91DN1 12 Q9Q9G5 |
| 670 747 747 | 156 252 290 290 | 387 541 5441 8442 | 899 1049 143 193 208 | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 |
| 67.3 67.3 67.3 | 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 633.54 633.54 633.54 633.53 | |
| | . w w w w . | # # # # # # # # # # # | # # # # # # # # # # # # # # # # # # # | |
| 118 118 100 100 | 4 G G G G G | 35876 | 33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 |

ALIGNMENTS

| PRELIM PRELIM 1033 (TrEMB 1033 (TrEMB 1033 (TrEMB 1033 (TrEMB 1050CUS elon 1050CUS elon 1053046; 1044 AA. 1119U 1044 AA. 1144 AA. | T 1 0 0 DEBLIMINARY; PRT; 1044 AA. 108DIH0; PRELIMINARY; PRT; 1044 AA. 108DIH0; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Multiding efflux transporter. | Pacteria; Cyanobacteria; Chrococcales; Synechococcus. Bacteria; Cyanobacteria; Chrococcales; Synechococcus. NGBL TaxID=32046; [1] SEQUENCE FROM N.A. STRAIN=BP-1; MEDLINE=22225144; PubMed=12240834; MARAMURA Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Makamura Y., Kaneko T., Sato S., Ikeuchi M., Matsuno A., Iriguchi M., Matsuno M., Matsuno A., Nakazaki N., Kiyokwa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Matsuno S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; BMBJ, AP005374; BAC09170.1; Complete protecome. Complete protecome. Complete protecome. | 75.0%; Score 39; DB 16; Length 1044; 63.6%; Pred. No. 24; Vative 2; Mismatches 2; Indels 0; Gaps |
|--|--|---|--|
| SULT 1 DIHO OBDIHO; OBDIHO; O1-MAR-20 01-MAR-20 01-MAR-20 01-MAR-21 01-MAR-21 01-MAR-20 01-MAR- | T 1 0 08DIH0 PRELIMINARY, 09BIH0; 01-MAR.2003 (TERMELrel. 23, Cr 01-MAR.2003 (TERMELrel. 23, La 01-MAR.2003 (TERMELrel. 23, La MULLiddug efflux transporter. | Yanechococcus elongatus (Thermosynech Bacteria; Cyanobacteria; Chrococcale NCB TaxID=32046; ILI — SANDENCE FROM N.A. STRAIN=BP-1; MEDLINE=22225144; PubMed=12240834; MEDLINE=22222144; PubMed=12240834; MARAMURA Y., Kaneko T., Sato S., Ikeu Watanabe A., Iriguchi M., Kawashima K. Kiyokawa C., Kohara M., Matsumoto M., Shimmpo S., Sugimoto M., Takeunico M., "Complete genome structure of the the Thermosynechococcus elongatus BP-1."; DNA Res. 9:123-130(2002). Complete proteome. Complete proteome. Complete proteome. | 75.0%; Similarity 63.6%; 7; Conservative |

|||:|| |: || 843 EEVLPNGIGYS 853 셤

1 EEVVPXGMSYS 11

ò

ö

PRT; PRELIMINARY; RESULT 2 Q98FX1 ID Q98FX1

387 AA.

us-09-909-164-10.rspt

```
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=972h-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-HF-2
                                                                                                                                                                                                                                            SPAC869.05C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8EWD4
Q8EWD4;
                                                                                                                                   Q9URY8;
                                                                                                              Q9URY8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matchee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                   RESULT 4
                                                                                      QBEWD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCOCCOS REPARED DE LA REPARED
용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum."; J. Bacteriol. 180:5003-5009(1998).

EMBL; APO83072; AAC62699.1; -.
InterPro; IPR000515; BPD transp.
InterPro; IPR001689; WP40.
                                                                                                                                                                                                                                                                                                            Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Simpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Simpo S., Sugimoto M., Domplete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."; DNA Res. 7:31-338(2000).

EMBL; AP003002; BAB50445.1; -.
InterPro; IPR00293; Peptidase M20.
Pfam; PF01546; Peptidase M20.
Pfam; PF01546, Peptidase M20; I.
Hydrolase; Complete protecome.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=B;
MEDINE=98422450; PubMed=9748430;
Schleper C. DeLong B.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 73.1%; Score 38; DB 16; Length 387; Local Similarity 60.0%; Pred. No. 13; Conservative 2; Mismatches 2; Indels
                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 54.5%; Pred. No. 1.5e+02;
6; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00320; WD40; 2.
PROSTIR; PS00402; BPD TRANSP_INN MEMBR; 1.
Hypothetical protein; Repeat; WD repeat
SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     074056;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 367.1 kDa protein.
                     (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 3472 AA
                                                                                                                                   Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                         MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| :| ||||
367 DEAIPHGMSY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 REVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cenarchaeum symbiosum.
                                                                                         Hippurate hydrolase.
MLR3583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                      STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cenarchaeum.
NCBI_TaxID=46770;
                     01-0CT-2001
01-0CT-2001
                                                                 01-OCT-2001
                                                                                                                                                                                                                            (1)
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     074056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                074056
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

1 EEVVPXGMSYS 11

ò

..

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki Y., Ishikiwa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshimo C., Horino A., Shiba T., Sasaki T., Hattori M.;
'The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL, AP004171; BAC44062.1;
Complete proteome.
SEQUENCE 1123 AA; 123636 MW; A4D707330E3DB4AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                 Aunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AL132779; CAB60015.1; -.
GeneDB SPONDe; SPAC869.05c; -.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulph_transpt.
Pfam; PF00316; Sulfate transp; 1.
Pfam; PF00316; Sulfate transp; 1.
PRGRAMA; TICROROBLS; BILP; 1.
PROSITE; PS50801; STAS; 1.
SEQUENCE 840 AA; 93517 MW; ED4833E162B69077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_тахID=28227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.2%; Score 37; DB 16; Length 1123; 70.0%; Pred. No. 70; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.2%; Score 37; DB 3; Length 840; 77.8%; Pred. No. 51; ive 1; Mismatches 1; Indels
                                                                                                                                                           Schizosaccharomyces pombe (Flssion yeast).
Bukaryota, Pungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                 Last sequence update)
Last annotation update)
840 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22354719; PubMed=12466555;
                                     01-WAY-2000 (TrEMBLrel. 13, 01-WAY-2000 (TrEMBLrel. 13, 01-WAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2003 (TrEMBLrel. 23, 01-WAR-2003 (TrEMBLrel. 23, 01-WAR-2003 (TrEMBLrel. 23,
                                                                                                              Probable sulfate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 77.8
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 70.0 hes 7; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658 EYVPMGLSYS 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYPE 2560 paralog, 57%.
MYPE2710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 VVPQGMSYA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

```
Similar to glioma tumor suppressor CANDIDATE region gene
                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8BK35
Q8BK35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        040129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
040129
11D 040122
AC 04012
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
CO SELEAT
OC SELEAT
OC ABTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08BK35
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCOCOS DE LA SERVICIO DEL SERVICIO DEL SERVICIO DE LA SERVICIO DEL SERVICIO DEL SERVICIO DE LA SERVICIO DEL SERVICIO DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              È
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol-MAR-2002 (TrEMBLrel. 20, Created)
Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 20, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
GLTSCR2 OR AW536441.
Buts musculus (Mouse).
Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 11; Length 471;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 11; Length 484;
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUR-Liver;
Strausberg R.;
Strausberg R.;
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AAH25810.1;
MGD; MGT:218441; GltsGr2.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Straubberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017637; AAH17637.1;
MGD; MGI:2154441; Gltscr2.
SEQUENCE 484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 471 AA; 54506 MW; BODA685C374A9760 CRC64;
                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 54.5 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                       471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 EVIPAGASYN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||:| | ||:
EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBBTX4
QBBTX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8VD18
Q8VD18;
                                                                                                                                                                                                                                                                                                       GLTSCR2
                                                                                                                                             Q8R126;
                                                                                                                    Q8R126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                     RESULT 6
Q8R126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08VD18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8BTX4
                                                                                                                                                PAC OCC OC DIT IN THE REAL SO SEE THE REAL SEE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

```
SECUENCE FROM N.A.

STRAIN=NOD; TISSUE=Thymus;

STRAIN=223346891; PubMed=12466851;

The MEDLINES.223546891; PubMed=12466851;

The RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs.";

Nature 420:563-573 (2002)

EMBL; AK088461; BAC40367.1; -.

SEQUENCE 484 AA; 55806 MW; B3056425B5EECADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Pituitary;

MEDLINS=223546813; PubMed=1246681;

The FANYOM Consortium
The FANYOM Consortium
The FANYOM Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,70 full-langh cNNAs.";

"Analysis of the Mouse transcriptome based on functional annotation of Mature 420:563-573 (2002).

EMBL; AK077341; BAC36760.1;

EMBL; AK077341; BAC36760.1;

SEQUENCE 484 AA; 55792 MW; EB67949BCBE92D44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q40129;
01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-NOV-2996 (TEMBLrel. 23, Last annotation update)
1-NOPCHPETICAL 25.2 kDa protein precursor.
1-YOOPCHPETICAL (TEMBLO).
1-YOOPCHPETICAL (TINDATO).
1-YOOPCHPETICAL (TINDATO).
1-YOOPCHPETICAL (TINDATO).
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                  Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 45; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 45; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
81milar to glioma tumor suppressor CANDIDATE region gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EVVPXGMSYS 11
protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
```

```
SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Head;

MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium.

The RIKEN Genome Exploration Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

Nature 420:563-573(2002).

EMBL; AK028258; BAC25846.1; -.

SRQUENCE 495 AA; 55358 WW; B6A22A093C114752 CRC64;
                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
DNA binding protein (Fragment).
DN451B15.2.
Bune asplene (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCTI.
Plasmodium falciparum.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 11; Length 495;
Pred. No. 75;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%; Score 35; DB 4; Length 556; 66.7%; Pred. No. 86; 1:ve 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tubby B.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; Z98050; CAB10847.1; -. NON TER 1 SEQUENCE 556 AA; S9059 MW; ECB00E4033FB2528 CRC64;
                              01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
CDNA F131891 FIS.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 AA.
 495 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                    63.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7's
Lagan 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 ERIVPMGISPS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 BEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 VVPAGLTYS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choline transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             043733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BH83,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BH83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BH83
 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88888888888888
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                             SEQUENCE FROM N.A.

STAIN-FP36; TISSUE-Pistil;

K MEDLINE-95375.23; PubMed=7647301;

Milligan S.B., Gasser C.S.;

"Nature and regulation of pistil-expressed genes in tomato.";

I Plant Mol. Biol. 28:691-711 (1995).

E RMB.; U20592; AAA80497.1; -1.

R InterPro; IPR002160; Kunitz_legume.

R Pfan, PR00197; Kunitz_legume.

R Pfan, PR00197; Kunitz_legume.

R Probom; PD000891; Kunitz_legume; 1.

R PRODIN; SM00453; STI, 1.

R PROSITE; PS00283; SOVBEAN KUNITZ; 1.

H Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                               Score 35; DB 10; Length 225; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 425;
                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";

Science 282:2012-2018(1998).

BMBL, 281109; CABO224.1;

WormPep; R10012.10; CE12690.

InterPro; IPR000719; Prot_kinase.

Prodom; PD000001; Prot_kinase; 1.

Propom; PROSTIT; PSC011; PROTEIN KINASE_DOW; 1.

ATP-binding; Transferase.

SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                                                  SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 50.0%; Pred. No. 64; 5; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last seq 01-MAR-2003 (TrEMBLrel. 23, Last anno R10012.10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | | | | : |:
32 DEVVPNGKTYA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 EQIVPGGLQY 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R10D12.10.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
 NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XVK4
```

RESULT 11 Q9XVK4

ð 셤 ö

Gaps

ö

Best Loca Matches

δ 셤 RESULT 12 Q8C1D7

ö

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                    ö
                         Plasmodium (), Gliuzman I.Y., Goldberg D.B.,
Plasmodium falciparum choline transporter (PfSCT1) gene.",
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AX007374; AAK14818 11; -:
EMBL; AX007373; AAK14818 11; -:
InterPro; IPR002123; Acyltransferase.
Pfam; PR01553; Acyltransferase; I.
SMART; SM00563; Plac; 1.
SMART; SM0563; Plac; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SCTI...
Plasmodium falciparum.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
N.SI.TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;
"Plasmodium falciparum choline transporter (Pf5CT1) gene.";
submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY007372; AAC14816.1; -:
EMBL; AY007375; AAG17947.1; -:
InterPro; IPR002123; Acyltransferase.
Pfam, PF01553; Acyltransferase; 1.
SEQUENCE 583 AA; 66917 MW; 2B2BFAE3E3395E049 CRC64;
                                                                                                                                                                                 Query Match 67.3%; Score 35; DB 5; Length 583; Best Local Similarity 55.6%; Pred. No. 90; Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
67.3%; Score 35; DB 5; Length 583;
Best Local Similarity 55.6%; Pred. No. 90;
Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         583 AA.
                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                 227 IIPVGLSYS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 IIPVGLSYS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VVPXGMSYS 11
                                                                                                                                                                                                                                               3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                   Choline transporter.
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Q9BHA5
                                                                                                                                                                                                                                                                                                                       RESULT 15
Q9BHA5
 ద
                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

Search completed: December 22, 2003, 17:51:29 Job time: 25.2667 secs

c virus c virus c virus c virus c virus c virus

Hepatitis

: virus

C virus C virus C virus C virus C virus C virus C virus C virus C virus C virus C virus C virus C virus

```
/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "D-form residue"
                                                                                                                                                                                                                                      ABB60536
ABB80538
ABB80538
ABB80540
ABB80540
ABB80541
ABB80544
ABB80544
ABB80544
ABB80545
ABB80554
ABB80555
ABB80555
                                                                                                                                                    ABB80563
ABB80564
ABB80565
ABB80566
ABB80567
ABB80568
ABB80555
ABB80531
ABB80521
ABB80522
ABB80526
ABB80526
ABB80526
ABB80528
ABB80529
ABB80529
ABB80529
ABB80529
ABB80529
ABB80563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80523 standard, peptide, 11
 19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
 Synthetic
 results predicted by chance to have a . to the score of the result being printed, of the total score distribution.
                                                                             December 22, 2003, 16:41:00 ; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                          A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                        1107863
            5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                               1107863 seqs, 158726573 residues
            GenCore version (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80527
ABB80527
ABB80558
ABB805560
ABB80537
ABB80541
ABB80546
ABB80550
ABB80550
                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of res
score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
                                                                                                                                                1 BEVVPXGMHYS(11)
                                                                                                                           US-09-909-164-11
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333333333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                        protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                       Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.4
96.4
96.4
96.4
87.5
885.7
85.7
                                                                                                                                                                                                                                      Total number of
                                                                                                                              Title:
Perfect score:
                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0000044444
4444000000
                                                           .
                                                        OM protein
                                                                                                                                                                                                                                                             88
                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                             Minimum Maximum
                                                                                Run on:
```

Result 8 ô

Gaps

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                           Length 11;
                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                         Score 54; DB 23; 1 Pred. No. 0.00053;
                                                                                                                                                                                                                 96.4%; Scor.
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brunck TK;
                                                                                The sequence represents a peptide hepatitis C virus (HCV) protease i
                                                                                                                                                                                                                                                                                                                                                                                 ABB80558 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
                                                         Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                 1
                                                                                                                                                                                                                                                                                                           1 EBVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                 1 REVVPXGMHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-361643/39.
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                 11 AA;
                              virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                             ABB80558;
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virucide
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                      ABB80556
                                                                                                                                                                                                                                                                                                                                                                                                  CCXBX5151478XBXBXBXBX515151515151548X8X8XBXBXXXX
 ***************
                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha *tetoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                          DB 23; Length 11; 0.00053;
                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                       Match 96.4%; Score 54; DB Local Similarity 100.0%; Pred. No. 0.0 (es 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck TK;
                                                         Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB80527 standard; peptide; 11 AA.
                                                                                                                                                                     Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000; 2000US-220101P.
 21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
/note=
                                                                                                                                                                                                                                                                                                                                                                                                  EBVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC
                             (CORV-) CORVAS INT INC
                                                          Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-361643/39.
                                                                                    WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                              11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                            virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                         Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virucide
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                          d
```

```
is useful for treating disorders associated with hepatitis C virus.
                      Sequence
                                                             Matches
                                                                                                                                  RESULT 5
  SXS
                                                                                                    셤
                                                                                  ò
                                                                                                                                                                 ö
                               pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                         "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HcV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HcV protease. A pharmaceutical composition comprising the peptide as an active ingredient
           ŏ
invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A
                                                                                                      Gapa
                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40.
                                                                                                      ö
                                                                               96.4%; Score 54; DB 23; Length 11;
100.0%; Pred. No. 0.00053;
ive 0; Mismatches 0; Indels
                                                                                                   0; Indela
                                                                                                                                                                                                                                                                                                                                                       'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                        note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                            "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                              ABB80560 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                        (first entry)
                                                                                                     11; Conservative
                                                                                                                                     EEVVPXGMHYS 11
                                                                                                                         1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-361643/39
                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              Θ
                                                             11 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200208251-A2
                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lim-wilby M,
                                                                                                                                                                                                                                       08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2002
                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                    ABB80560;
                                                                                                                                                                                                                                                                                            virucide.
                                                             Sequence
                                                                                 Query Match
                                                                                                    Matches
 88888888
                                                                                                                                           셤
                                                                                                                                                                                                          ò
```

```
"Norvalyl carbonyl forming keto-amide linkage with residue ?"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a peptide compound of the invention having hepptides C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17
                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                      1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 11;
                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                      Length
                                    DB 23; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 23;
Pred. No. 0.0051;
0; Mismatches 1;
                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "D-form residue"
                                    Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŢĶ;
                      96.4%; Sco.
100.0%; Pre
                                                                                                                                                                                                                                                   ABB80537 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                 Ξ
                                                                                                                                                    H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Levy OE,
                                                                                                                                                  1 EEVVPXGMHYS
                                                                                                               1 REVVPXGMHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-361643/39
                                                      Similarity
11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lim-wilby M,
                                                                       11;
                                                                                                                                                                                                                                                                                                                                08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                            ABB80537;
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                virucide
```

ò

ò 셤 08-OCT-2002

ABB80541;

Synthetic

virucide.

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                      "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30.
                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 23;
Pred. No. 0.008;
0; Mismatches 1
                                                                                                                                                                                                                      'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                     "C-terminal amide"
                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80550 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186.06
                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2001, 2001WO-US23169
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ።
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||||| |||
EEVVPXGTHYS 11
                                                                                                                                                                                                                                                                                      11
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 REVVPXGMHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus protease
                                                                                                                                                                                                                                                                                                                                     WO200208251-A2
                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                       Modified-site
                                           08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB80550;
               ABB80546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
გ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                     "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 23; Length 11;
Pred. No. 0.0051;
0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                     /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                      "D-form residue"
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŢĶ;
                                                                                                              ABB80541 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2001; 2001WO-US23169
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ħ
EEVVPXGMHYS 11
                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVVPXGQHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide
activity usefu
                                                                                                                                                                                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim-wilby M,
```

31-JAN-2002

ö

Gaps

ö

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

ABB80546 standard; peptide; 11 AA.

RESULT 7 ABB80546 ID ABB8

ઠે 셤

Sequence

us-09-909-164-11.rag

```
Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                85.7%;
90.9%;
                                                                                                                19-JUL-2001; 2001WO-US23169
                                                                                                                                         21-JUL-2000, 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 BEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGSHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                  (CORV-) CORVAS INT INC
                                                                                                                                                                                        Lim-wilby M, Levy OE,
                                                                                                                                                                                                                 WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 9
 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                             WO200208251-A2
                                                                                                                                                                                                                                                                      virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200208251-A2
                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                      31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB80555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB80555
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                   "Norvaly1 carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus, HCV, serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 23; Length 11;
Pred. No. 0.008;
0; Mismatches 1; Indels
                                                'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "N-terminal acetyl"
                                                                                                                                      /note= "C-terminal amide"
                                                                                                             'note= "D-form residue"
                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                            Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80554 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.7%;
90.9%;
                                                                                                                                                                                                                                         21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                 19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||||| |||
EEVVPXGSHYS 11
                                                                           /note=
                                                                                                                                                                                                                                                                                            Levy OE,
                                                                                                                                                                                                                                                                CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                   WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AA;
                                                                                                Misc-difference
                                                                                                                                                              WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                       virus protease
                                   Modified-site
                                                                                                                         Modified-site
                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                           Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-2002
                                                                                                                                                                                        31-JAN-2002
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB80554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
```

ABB80554 RESULT

셤 ઠે

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 23; Length 11;
Pred. No. 0.008;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "N-terminal acetyl"
                                                                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "C-terminal amide"
/note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80555 standard; peptide; 11 AA.
```

ô

Novel

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #12
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                 Score 46; DB 23; Length 11;
Pred. No. 0.02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80532 standard; peptide; 11 AA
                                                                                                                Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                   82.1%;
ilarity 90.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      1 REVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                       1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                       1 BEWVPXGGHYS
               WPI, 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 9
                                                                                                                                                                                                                                                                                     11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease
                                                                                virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virue
8
                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                   The sequence represents a peptide compound of the invention having the peptides of the. Inchaints C virue (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                        ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C bease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 23; Length 11;
Pred. No. 0.008;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brunck TK;
                                                                                                                                                 Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                     Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residue
                                                                                                                                                 Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2000; 2000US-220101P
                                               19-JUL-2001; 2001WO-US23169.
                                                                                21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .9-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Levy OB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORV-) CORVAS INT INC
                                                                                                                  (CORV-) CORVAS INT INC
                                                                                                                                                 Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEVVPXGSHYS
                                                                                                                                                                                   WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AA;
                                                                                                                                                                                                                                                      virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2002.
               31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

Matches

ઠે 셤 RESULT 11 ABB8053

Gaps

ö

```
Location/Qualifiers
                                                                                                                                                                                                                                                                                      ŦĶ;
                                                                                                                 ABB80521 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                              Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                      Brunck
                                                        82.1%;
90.9%;
                                                                                                                                                                                                                                                      19-JUL-2001, 2001WO-US23169.
                                                                                                                                                                                                                                                                 21-JUL-2000; 2000US-220101P.
                                                                                                                                     (first entry)
                                                                   10; Conservative
                                                                             1 EEVVPXGMHYS 11
                                                                                       ដ
                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                      Levy OE,
                                                                                   BEVVPXGGHYS
                                                                                                                                                                                                                                                                                                WPI; 2002-361643/39.
                                                             Local Similarity
                                             11 AA;
                                                                                                                                                                                                                                                                                                                    virus protease
                                                                                                                                                                                                                                  WO200208251-A2
                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                     Lim-wilby M,
                                                                                                                                     08-OCT-2002
                                                                                                                                                                                                                                            31-JAN-2002
                                                                                                                                                                         Synthetic.
                                              Sequence
                                                        Query Match
                                                                                                                                                               virucide.
                                                                  Matches
                                                                                                      RESULT 13
                                                                                                           ABB8052
*8888888888
                                                                             ઠે
                                                                                      셤
```

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide
        DB 23; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.4%; Score 45; DB 23; Length 11; 90.9%; Pred. No. 0.031; tive 0; Mismatches 1; Indels
                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
      Score 45; DB 23;
Pred. No. 0.031;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue 7"
                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Norvalyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                     ABB80522 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brunck
      90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                (first entry)
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                  1 EBVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ,
                                                                                                          EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levy
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
tes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lim-wilby M,
                                                                                                                                                                                                                                                                                              08-OCT-2002
                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                         ABB80522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity
        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                          Best Local
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                    å
                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                       ö
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1
                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                             Score 46; DB 23; Length 11;
Pred. No. 0.02;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                       1,
                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "C-terminal amide"
```

ö

Gaps

ö

11

셤 ઠે

Ä

1

Sequence

1 EEVVPXGMHYS 11

us-09-909-164-11.rag

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                    /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 23; Length 11;
Pred. No. 0.031;
0; Mismatches 1; Indels
                                                                                                                                                                                                                            'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                               'note= "D-form residue"
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brunck TK;
              ABB80524 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-220101P
                                                                    08-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                       WO200208251-A2
                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002.
                                                                                                                                                                    Synthetic.
                                         ABB80524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
ABB80524
```

ö

Gaps

ö

Search completed: December 22, 2003, 17:41:01 Job time : 32.4667 secs

ઠે g 4

۲.

```
Sequence 4794, Ap
Sequence 21444, A
Sequence 19, Appl
Sequence 2, Appli
Sequence 2615, A
Sequence 37844, A
Sequence 3784, A
Sequence 3950, Appl
Sequence 23, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                   December 22, 2003, 16:37:03 ; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Seq
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-134-001C-4794

US-09-252-991A-21444

US-08-821-119-19

US-08-821-118-2

US-08-252-991A-26615

US-09-252-991A-27834

US-09-252-991A-27834

US-09-134-01C-3950

US-08-995A-3

US-08-995A-3

US-08-995A-3

US-08-995A-3

US-08-134-01C-3950

US-08-134-01C-3950

US-08-46-44-4

US-08-46-517-21

US-08-246-361A-21

US-08-246-361A-22

US-08-246-361A-22

US-08-246-361A-22

US-08-246-361A-22

US-08-246-361A-22

US-08-246-361A-22

US-08-46-517-6

US-08-46-517-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-909-164-11
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
666.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \begin{array}{c} \mathbf{m} \, \mathbf{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ģ
```

| Sequence 6, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 24, Appli Sequence 26, Appli Sequence 27, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli | SEQUENCES RELATING TO STAPHYLOCOCCU | Length 1037; ; Indels 0; Gaps 0; | SEQUENCES RELATING TO PSEUDOMONAS |
|---|--|--|---|
| 291 5 PCT-US93-05000-6 292 2 US-08-464-517-23 292 2 US-08-246-361A-6 292 2 US-08-246-361A-2 292 3 US-08-246-3772-23 292 5 PCT-US93-05000-23 295 5 US-08-467-72-893A-8 295 1 US-08-47-120-8 295 2 US-08-464-517-19 295 2 US-08-464-517-19 295 2 US-08-464-517-20 295 3 US-08-463-3772-19 295 3 US-08-463-3772-19 295 3 US-08-460-744-2 | ALIGNMENTS 09134001C 1 and AMINO ACID DIS FOR DIAGNOSTICS 5/09/134,001C 5/1064,964 60/055,779 | ocus epidermidis 69.6%; Score 39; DB 4; 63.6%; Pred. No. 20; ative 2; Mismatches 2: 11 | US/09252991A eld et al. C ACID AND AMINO ACID NOSA FOR DIAGNOSTICS A US/09/252,991A 02-18 02-18 18 US 60/094,190 |
| 32 57.1 32 57.1 | SULT 1 -09-134-001C-4794 Sequence 4794, Application US/ Beatant No. 6380370 APPLICANT: Lynn Doucette-Stamm TITLE OF INVENTION: NUCLEIC ARTITLE OF INVENTION: EPIDERMIN FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US- FRICH APPLICATION NUMBER: US- PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 RECOR FILING DATE: 1997-11-08 RECORDER OF SEQ ID NOS: 5674 LENGTH: 1037 TYPE: PRT | ISM: -001C atch cal S 1 | RESULT 2 US-09-252-991A-21444 Sequence 21444, Application US/ Patent No. 6517795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield TITLE OF INVENTION: NUCLEIC AG TITLE OP INVENTION: NUMBER: US FILE REFERENCE: 1999-02-19 FRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 21444 LENGTH: 856 |
| 24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | RESULT 1 US-09-134-001C ; Sequence 479; ; PARENT NPO. 6; GENERAL INPO. ; TITLE OF IN ; FILE REFERE ; CURRENT APP. ; PRIOR FILIN ; PRIOR FILIN ; PRIOR FILIN ; PRIOR FILIN ; NUMBER OF S; ; SEQ ID NO 47; ; LENGTH: 10; ; TYPE: PRI | ; ORGANISM US-09-134-00 Query Matches Matches Oy Db 19 | RESULT 2 US-09-222-99 ; Sequence 2; Patent No.; Patent No.; Patent No.; Patent No.; PITER OF TITER OF |

```
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                ö
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Holm, Kaj Andre
APPLICANT: Rasmussen, Grethe
APPLICANT: Rasmussen, Grethe
APPLICANT: Halkier, Torben
APPLICANT: Lehnbeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
UNDBER OF SEQUENCES: 23
CORRESPONDENCES: 23
CORRESPONDENCES: ADDRESS:
ADDRESSEE: 405 Lexington Avenue
CITY: New York
STARTE: NY
COUNTRY: USA
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 2; Length 600;
Pred, No. 1e+02;
                                                        Score 37; DB 4; Length 856;
Pred. No. 40;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: 1980 MWINDER: US/08/821,119
FILING DATE: 1987 MAR. 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 31,728
TELECOMMUNICATION: INPORMATION:
TELECOMMUNICATION: INPORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                     Sequence 19, Application US/08821119
Patent No. 5821104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-821-118-2
; Sequence 2, Application US/08821118
; Patent No. 5989889
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                        Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 600 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10174
COMPUTER READABLE FORM:
                                                                                                                                    1 REVVPXGMHY 10
                                                                                                                                                                      64 EAVVPGGEHY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VPKGWHYS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-821-119-19
                                                                                                                                                                                                                                                       US-08-821-119-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                      ઠે
                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

```
Sequence 26615, Application US/09252991A

Retent No. 6551795

GRNERAL INPORMATION:

GRIERAL INPORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TILLE REPERENCE: 107136.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1988-02-18

PRIOR FILING DATE: 1988-02-18

RIOR FILING DATE: 1988-02-18

RIOR APPLICATION NUMBER: US 60/094,190

RIOR APPLICATION NUMBER: US 60/094,190

RENOR FILING DATE: 1988-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26615
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDASE
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER. NO. 59898890 No. 5989889disk of No. 5989889th America, Inc. STREET: 405 Lexington Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 2; Length 600;
Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.9%; Score 33; DB 4; Length 277; 63.6%; Pred. No. 70; 1.1ve 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OMPUTER: IBM Comparible
OMPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OFFICATION UNDER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAMB: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REPRENCE/DOCKET NUMBER: 33,728
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 18-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i TYPE: PRT
j ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VPKGWHYS 38
                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-26615
                                                                                                                                                                                                                                                             ZIP: 10174
                                                                                                                                                                                                                 STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-821-118-2
```

```
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENEUR: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/08580988A
Patent No. 5856161
GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: For Its Use
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCES: 27
CORRESPONDENCES: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%; Score 32; DB 4; Length 70; 62.5%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Houston
STATE: Texas
COUNTRY: USA
ZUP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIPICATION: DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REPERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELECHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               no
or: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: protein POTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no
FRAGMENT TYPE: 3
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                  Sequence 79834, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36, Application US/09724864

Patent No. 6380362

GENERAL INFORMATION:

APPLICANT: Watson, James D

APPLICANT: Watson, James D

APPLICANT: Watson, James G

TITLE OF INVENTION: Polynucleotides and methods for their use.

TITLE OF INVENTION: by the polynucleotides and methods for their use.

FILE REFERENCE: 11000.1050U1

CURRENT FILING DATE: 2000-11-28

PRIOR PILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FRRESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33, DB 4; Length 385;
Pred. No. 1e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 4; Length 747;
Pred. No. 2.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3950, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 44.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4
Matches 5; Conservative
         1 BEVVPXGMHYS 11
                                                                 48 EETVPGGGHTS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 EILPAALHY 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |:|||
627 PGGLHYS 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 PXGMHYS 11
                                                                                                                                                                                        US-09-252-991A-27834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-134-001C-3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rat
US-09-724-864-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-724-864-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 36
LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
      ઢ
                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
```

```
Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-460-694-4
  APPLICANT:
                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                ö
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 2; Length 126;
Pred. No. 46;
1; Mismatches 2; Indels
                                       57.1%; Score 32; DB 2; Length 102; 60.0%; Pred. No. 37; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                    Sequence 3, Application US/08879995A
Patent No. 5985606
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
CLASSIFICATION TATA:
APPLICATION NUMBER: DF.0995A
FILING DATE:
APPLICATION NUMBER:
RILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: BILLINGS, LUCY J.
REGISTRATION INPORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09215096
Patent No. 6008194
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acide TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                     Query Match 57.1
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.1
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                       1 EEVVPXGMHY 10
                                                                                                                                                          24 BEVFPLAMNY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1:||| | |
28 EQVVPGGGH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 REVVPXGMH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: GenBank
CLONE: 163590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
    US-08-580-988A-23
                                                                                                                                                                                                                                        US-08-879-995A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-879-995A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-215-096-3
                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                       ð
                                                                                                                                                          셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08460694

Patent No. 5858655

GENERAL INFORMATION:

TILE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMM PC Compatible
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 3; Length 126;
Pred. No. 46;
1; Mismatches 2; Indel8
                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURENT APPLICATION NUMBER: US/09/215,096
FILING DATE:
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 1104 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRANCE/DOCKT NUMBER: PF-0326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66./
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1:||| | |
28 EQVVPGGGH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 REVVPXGMH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: GenBank
; CLONE: 163590
US-09-215-096-3
```

```
20 BEVPPLAMNY 29
                                                                                                            US-07-667-711B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-193-977-7
                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4 Application US/08460744

Fatent No. 6107541

GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1100 New York Avenue, N.W., Suite 600
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.1%; Score 32; DB 3; Length 152; Best Local Similarity 60.0%; Pred. No. 57; Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: MCCONCATN, RVABER: 35,279
REFERRNCE/DOCKET NUMBER: 35,279
REFERRNCE/DOCKET NUMBER: 35,279
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.1%; Score 32; DB 2; Best Local Similarity 60.0%; Pred. No. 57; Matches 6; Conservative 1; Mismatches
                                                          ATTORNEY AGENT INFORMATION:
NAME: MCCONathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCETORY STATEMER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ 1D NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 152 amino acids TYPE: amino acid STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 BEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 BEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                            US-08-460-694-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-460-744-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

EEVVPXGMHY 10

```
TITLE OF INTERNAL INCOME.

SERVING THE ACTOR OF THE ACTOR
```

```
us-09-909-164-11.rai
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/193,977
FILING DATE: US/08/193,977

ATTORNEY/AGENT NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0016
FELECOMONICATION INFORMATION:
FELECOMONICATION INFORMATION:
FELECOMONICATION INFORMATION:
FELECOMONICATION INFORMATION:
FELENCE CHARACTERISTICS:
F
```

us-09-909-164-11.rapb

```
December 22, 2003, 16:40:14; Search time 20.8667 Seconds (without alignments) 98.451 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. / Gyn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/PCUB_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

/ Cyn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                696363 seqs, 186758610 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                         US-09-909-164-11
56
1 REVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published
                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                  Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | 2319, Ap | 126, App | 4919, Ap | 663, App | 4, Appli | 4, Appli | 4, Appli | 4, Appli | 241, App | 32076, A | 2076, Ap | 3, Appl | 114, App | 54, Appl | 2, Appli |
|-------------------------------|-----|--------------------|-------------------|--------------------|--------------------|-----------------|-----------------|-----------------|-----------------|-------------------|---------------------|--------------------|-------------------|-------------------|------------------|-----------------|
| Description | | Sequence 2319, Ap | Sequence | Seguence | Seguence | Sequence | Sequence | Seguence | Sequence | Sequence | Sequence 32076, | Sequence 2076, Ap | Sequence 53, Appl | Sequence | Sequence | Sequence |
| £ | | US-10-094-749-2319 | US-10-270-333-126 | US-09-738-626-4919 | US-09-866-050A-663 | US-10-029-120-4 | US-10-027-806-4 | US-10-034-623-4 | US-10-027-801-4 | US-10-199-820-241 | US-10-029-386-32076 | US-10-094-749-2076 | US-09-778-927A-53 | US-10-116-275-114 | US-09-919-497-54 | US-10-024-066-2 |
| ŭ | } ! | 12 | 15 | 10 | 11 | 12 | 14 | 14 | 15 | 12 | 12 | 12 | 0 | 12 | 10 | 14 |
| * Query Match Length DB | | 273 | 567 | 622 | 747 | 3472 | 3472 | 3472 | 3472 | 36 | 236 | 242 | 254 | 276 | 289 | 289 |
| Query March | | 58.9 | 58.9 | 58.9 | 58.9 | 58.9 | 58.9 | 58.9 | 58.9 | 57.1 | 57.1 | 57.1 | 57.1 | 57.1 | 57.1 | 57.1 |
| Score | | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 32 | 32 | 32 | 32 | 32 | 32 | 32 |
| Result | | 1 | 7 | 3 | 4 | 'n | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 |

t TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-094-749-2319

| Sequence 4, Appli Sequence 275, App Sequence 1315, Ap Sequence 24, Appl | 164, 36, | 15,15 | Sequence 10, Appl Sequence 80, Appl Sequence 52, Appl | 124 171 171 | 1119, 1276 | Sequence 10517, A Sequence 86, Appl Sequence 4, Appli Sequence 1, Appli Sequence 526, App |
|--|-------------------|--|---|---------------------------------------|--|---|
| | | US-09-252-088-15 US-10-340-792-16 US-09-252-088-15 US-10-340-792-15 | | | US-10-001-857-119 US-10-156-761-12762 US-10-106-698-6257 US-09-815-242-13489 US-09-815-242-13489 | US-09-815-242-10697 US-09-782-974C-86 US-09-943-798-4 US-09-885-453-1 US-10-017-161-526 |
| 42121 | | 12121 | 1 | | 44 61 15 15 | 121911 |
| 289 292 315 | 519 519 653 | 715 | 847 847 847 | 59 73 153 192 | 192 216 251 260 260 | 337 337 337 337 |
| 57.1 57.1 57.1 | 57.1 | 57.1 | 26.22 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8 | |
| 2222 | 0 0 0 0 0 0 0 | 1 0 0 0 0 1 0 0 0 0 | | 311111 | ###################################### | |
| 16 17 18 19 | 2220 | 25 2 2 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 9696 | 1 6 6 6 6 1 6 6 6 6 | 0 E E E E E | 44444 44444 |

ALIGNMENTS

MESULY 1

US-10094-749-2319

US-10-094-749-2319

Sequence 2319, Application US/10094749

Publication No. US20030219741A1

Publication No. US20030219741A1

APPLICANT: ISOGAI, TAKAO

APPLICANT: SOUIYAWA, TOWOYASU

APPLICANT: WAKAWATSU, I

APPLICANT: WAKAWATSU, I

APPLICANT: SATO, HIROYUKI

APPLICANT: SATO, HIROYUKI

APPLICANT: TANAWOTO, JUN-ICHI

APPLICANT: TSONO, YUUKO

APPLICANT: TRAE, RYOTARO

APPLICANT: TAMECHIKA, TCHIRO

APPLICANT: TAMECHIKA, TCHIRO

APPLICANT: TAMECHIKA, TCHIRO

APPLICANT: TAMECHIKA, TCHIRO

APPLICANT: MAGNIN, WASUHIKO

APPLICANT: NAGHARI, KENUI

APPLICANT: NAGHARI, COU-094, 749

CURRENT APPLICATION NUMBER: 107 2001-328381

PRIOR APPLICATION NUMBER: 2002-01-24

PRIOR PILING DATE: 2002-01-24

PRIOR PILING DATE: 2002-01-24

PRIOR PILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 3381

SEGFWARE: PALENTIN VET. 2.1

SEGOFWARE: PALENTIN VET. 2.1

SEGOFWARE: PALENTIN VET. 2.1

;

1; Indels

Length 622;

```
Sequence 4, Application US/10029120
| Publication No. US20030175708A1
| GENERAL INPORMATION:
| APPLICANT: Swanson, Ronald V.
| APPLICANT: Swanson, Rohert A.
| APPLICANT: Schleper, Christa
| TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS PROM CENARCHAEUM SYMBIOSUM
| FILE REFERENCE: DOORP. 002A
| CURRENT FILING DATE: 2001-12-21
| PRIOR PILING DATE: EARLIER FILING DATE: 1999-09-29
| NUMBER OF SEQ ID NOS: 123
| SOFTWARE: PASEEE for Windows Version 3.0
| SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.9%; Score 33; DB 12; Length 3472; Best Local Similarity 45.5%; Pred. No. 2.6e+03; Matches 5; Conservative 4; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                   Sequence 653, Application US/09866050A

Publication No. US20030040471A1

GENERAL INPORMATION:

APPLICANT: Watson, James D.

APPLICANT: Stream, Matthew

APPLICANT: Sleeman, Matthew

APPLICANT: Sleeman, Matthew

APPLICANT: Munble, Krishanand D.

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: and Methods for Their Use

FILE REFERENCE: 11000, 1011c4U

CURRENT APPLICATION NUMBER: US/09/866,050A

CURRENT PILIG DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 725

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.9%; Score 33; DB 11; Length 747; 71.4%; Pred. No. 5e+02;
                                                                                                            Score 33; DB 10;
Pred. No. 4.1e+02;
3; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                    ) TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-029-120-4
                                                                                                                 Query Match 58.9%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                              1 BEVVPXGM--HY 10
                                                                                                                                                                                                                                          46 BRIIPIGVPNHY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 PGGLHYS 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-866-050A-663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-10-029-120-4
LENGTH: 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cracchik, Anibal
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES;
TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
FILE REFERENCE: CLOOO733CON
CURRENT PAPLICATION NUMBER: US/10/270,333
CURRENT FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 198
SCOTTWAR OF SEQ IC Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                      Gaps
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.9%; Score 33; DB 15; Length 567; 83.3%; Pred. No. 3.7e+02; ive 0; Mismatches 1; Indels
                 Query Match 58.9%; Score 33; DB 12; Length 273; Best Local Similarity 71.4%; Pred. No. 1.7e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: CATAI, KEIKO
APPLICANT: YOKOI, HARCHIKO
APPLICANT: YOKOI, HARCHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, MASATO
APPLICANT: OZAKI, AKO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERRNCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 4919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4919, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  Sequence 126, Application US/10270333
Publication No. US20030092124A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.5.
                                                                                                                                                  151 PGGLHYS 157
                                                                                                                      5 PXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Drosophila
US-10-270-333-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 PSGMHY 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-738-626-4919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 126
LENGTH: 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                      δ
                                                                                                                                                                 셤
```

Gaps

ö

Gaps

```
RESULT 10
US-10-029-386-32076
                                                                                                                                                                                                                                                                  SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                      APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REPERENCE: DCORP.002A
CURRENT PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Swallon, Robert A.
APPLICANT: Statemen, Robert A.
APPLICANT: Feldman, Robert A.
TITLE OF INVESTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
TILLE REFERENCE: DCORP.002A
CURRENT PELING DATE: 1090-122
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR APPLICATION NUMBER: 69/408,020
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 14; Length 3472;
Pred. No. 2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 14; Length 3472;
Pred. No. 2.6e+03;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                      Sequence 4, Application US/10027806
Publication No. US20020160476A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10034623
Publication No. US20020198365A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/10027801
; Publication No. US20030054364A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Cenarchaeum symbiosum US-10-027-806-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3472

FYPR: PRT

ORGANISM: Cenarchaeum symbiosum

US-10-034-623-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                             |:|:| |: |
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:| |: :|
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 45.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|:| |: |
2294 EDVIPRGISPS 2304
1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 BEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-10-027-801-4
                                                                                                                                    US-10-027-806-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-034-623-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
    ઠે
                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
Sequence 32076, Application US/10029386
| Publication No. US20030194704A1
| GRNERAL INFORMATION:
| APPLICANT: Penn, Sharron G.
| APPLICANT: Penn, Sharron G.
| APPLICANT: Hanzel, David R.
| APPLICANT: Hanzel, David R.
| TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL POR FILE REFERENCE: AECMICA.*.2
| CURRENT APPLICATION NUMBER: US/10/029,386
| CURRENT FILING DATE: 2001-12-20
| CURRENT FILING DATE: 2001-12-20
| NUMBER OF SEQ ID NOS: 34288
| SOFTWARE: Annomax Sequence Listing Engine vere. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Board of Trustees of the University of Illinois
APPLICANT: Brimiano, Thomas
APPLICANT: Chang, Bey-dih
APPLICANT: Roninson, Igor
TILE OF INVENTION: Methods and Reagents for Identifying Gene Targets for Treating
FILE REFERENCE: 99,216-U
CURRENT FILING DATE: 2002-09-23
NUMBER OF SEQ ID NOS: 314
SOFTWARE: Patentin version 3.0
SEQ ID NO 241
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,801
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASTER FILING DATE: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                     Length 3472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                   ; DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 1
Pred. No. 31;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-199-820-241
; Sequence 241, Application US/10199820
; Publication No. US20030180739A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                        i LENGTH: 3472
i TYPE: PRT
i ORGANIEM: Cenarchaeum symbiosum
US-10-027-801-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                   58.9%;
45.5%;
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.5.
Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|| |::|
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 REVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 REVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 EEVPPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-820-241
```

```
Sequence 53, Application US/09778927A

Sequence 53, Application US/09778927A

Patent NO. USZO020068342A1

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL

TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

FILE REFERENCE: 2786-01.60P

CURRENT APPLICATION NUMBER: US/09/778,927A

CURRENT PILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 81

SOFTWARE PATENTIN VET: 2.1

SEQ ID NO 53

LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRATURE:
NAME/KRY: misc_feature
| CACATION: (1)...(254 )
| OTHER INFORMATION: Xaa = any amino acid, unknown, or other US-09-778-927A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 BEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-116-275-114
US-09-778-927A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                        PATURE: PRT
ORGANIS:
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN LACENTA, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN BOIN AGRAN, SIGNAL = 3.5
OTHER INFORMATION: SKRESSED IN POTHER, SIGNAL = 3.5
OTHER INFORMATION: SKRESSED IN POTHER, SIGNAL = 3.5
OTHER INFORMATION: SKRESSED IN FORTAL LIVER, SIGNAL = 3.5
OTHER INFORMATION: SWISSPROT HIT: P15622, EVALUE 1.00e-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 12; Length 242;
Pred. No. 2.4e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 12; Length 236;
Pred. No. 2.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: STATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: HIO, YUUK
APPLICANT: HOO, YUUR
APPLICANT: HIO, YUUR
APPLICANT: TAMEGHIKA, KAORU
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: MAGHIKO
APPLICANT: WASHIKAMA, TSUTOMU
APPLICANT: WASHIKAMA, WAOYUKI
APPLICANT: WASHIKAMA, WAOWUKI
APPLICANTING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR PILING DATE: 2002-01-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2076, Application US/10094749
Publication No. US20030219741A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%;
illarity 60.0%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2076
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEVPPLAMNY 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 VVPAGLTYS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-094-749-2076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                             US-10-029-386-32076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

Gaps

ö

57.1%; Score 32; DB 9; Length 254; 60.0%; Pred. No. 2.5e+02; tive 1; Mismatches 3; Indels

```
Sequence 114, Application US/10116275

Publication No. US20030211476A1

GENERAL INPORMATION:

APPLICANT: Blan Pharmaceutical Technology

APPLICANT: Brayden, David

APPLICANT: Brayden, David

APPLICANT: Brayden, David

APPLICANT: Brayden, David

APPLICANT: Lambkin, Imelda

APPLICANT: Lambkin, Imelda

APPLICANT: Lambkin, Imelda

APPLICANT: Byrne, Daragh

APPLICANT: Byrne, Daragh

APPLICANT: Byrne, David

APPLICANT: Byrne, David

APPLICANT: Lambkin, Imelda

APPLICANT: Lambkin, LiBa

TITLB OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and

TITLB OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors

TITLB OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors

CURRENT APPLICATION UNDMESE: 2002-10-04

NUMBER OF SEQ ID NOS: 349

SOFTWARE: PatentIn version 3.1

SEQ ID NO 114

LENGTHER 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 12; Length 276;
Pred. No. 2.7e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 54, Application US/09919497; Patent No. US20020106662A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60..
Best Acas Similarity 60..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 EEVPPLAMNY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Homo sapiens
US-10-116-275-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-919-497-54
```

```
Sequence 2, Application US/10024066

Publication No. US20020166134A1

GENERAL INFORMATION:

APPLICANT: Field, Loren J.

APPLICANT: Pasumarchi, Kishore Babu S.

TITLE OF INVENTION: CARDIOMYCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

TITLE OF INVENTION: CARDIOMYCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

TITLE OF INVENTION: CARDIOMYCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

FILE REFERENCE: 7037-450

CURRENT APPLICATION NUMBER: US/10/024,066

PRIOR PILING DATE: 1099-06-18

PRIOR PILING DATE: 1999-06-18

PRIOR PILING DATE: 2000-06-19

PRIOR PILING DATE: 2000-06-19

WUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REPERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR PAPLICATION NUMBER: US 60/221,735
; PRIOR PILING DATE: 2000-07-31
; PRIOR PILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.0
; SOFTWARE: Patentin version 3.0
; SOFTWARE: PATENTING SAPIENTING SAPIENTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 14; Length 289;
Pred. No. 2.9e+02;
1; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.1%; Score 32; DB 10; Length 289; Best Local Similarity 60.0%; Pred. No. 2.9e+02; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.1%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 2
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-024-066-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EBVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| | |:|
74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 EEVFPLAMNY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-10-024-066-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

Search completed: December 22, 2003, 17:32:43 Job time: 21.9333 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

December 22, 2003, 17:24:36; Search time 9.06667 Seconds (without alignments) 116.675 Million cell updates/sec Run on:

US-09-909-164-11 56 1 BEVVPXGMHYS 11 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir 76:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| SUMMAKIES | Description | 7 ftsH proteinase ac | carbamoyl-phospl | | | hypothetical | hypothetical | conserved hyp | | | | | | 9 hypothetical prote | | | | hypothetical p | Sls1 protein | hypothetical | ATP-dependent | | | | | | | | 4 coenzyme F420-quin | himothopical article |
|-----------|----------------|----------------------|------------------|--------|--------|--------------|--------------|---------------|--------|--------|--------|--------|--------|----------------------|--------|--------|--------|----------------|--------------|--------------|---------------|--------|---------------|--------|--------|--------|--------|--------|----------------------|----------------------|
| S | | A72207 | F89892 | A42452 | AE2001 | 869046 | 538143 | D82618 | T02590 | H69194 | T24111 | G86430 | G69117 | C75538 | B75478 | T35025 | E69086 | C83903 | 858132 | T28717 | AF3286 | 854619 | B83607 | G82253 | G71542 | H81697 | 865811 | HODVLB | A69284 | A DOCE |
| | DB | | ~ | ~ | ~ | ~ | ~ | ~ | N | ~ | ~ | ~ | ~ | ~ | ~ | N | ~ | ~ | ~ | ~ | æ | ~ | ď | ~ | ~ | ~ | ~ | - | 7 | · |
| | Length | 308 | 1057 | 102 | 252 | 460 | 743 | 156 | 233 | 311 | 425 | 510 | 264 | 279 | 350 | 355 | 360 | 425 | 426 | 495 | 1028 | 156 | 367 | 441 | 466 | 466 | 487 | 514 | 534 | 17.2 |
| 4 | Query Match | 66.1 | 66.1 | 64.3 | 64.3 | 64.3 | 64.3 | 62.5 | 62.5 | 62.5 | 62.5 | 62.5 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 60.7 | 58.9 | 58.9 | 58.9 | 58.9 | 58.9 | 58.9 | 58.9 | 58.9 | 6 |
| | Score | 37 | 37 | 36 | 36 | 36 | 36 | 35 | 35 | 35 | 35 | 35 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | ć |
| | Result No. | - | 7 | ٣ | 4 | S | 9 | 7 | 8 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | č |

| DNA mismatch repai macrophage-stimula | C14B9.8 protein - L-shaped tail fibe | hypothetical 367K tachykinin B precu | heme exporter prot hypotherical prote | ribosomal protein | probable Thus prot hypothetical prote | cyclin D2 - rat cyclin D2 - rat | cyclin D2 - mouse cyclin D2 - human |
|--|---|---|--|-------------------------|--|------------------------------------|--|
| A69663 JC5061 | S44754 S36851 | T31308 A25905 | D71640 S57810 | E97120 T07215 | C95881 T25737 | JC4011 I58372 | A41984 A42822 |
| 77 | 0 0 | 0 0 | 2 2 | 0 0 | N N | n n | 0 0 |
| 627 | 1257 | 3472 | 197 | 233 | 270 283 | 288 288 | 289 289 |
| ە ە | م م | 9.4 | | | | -: -: | |
| 58 | 8 8 | 58 | 57 | 57.1 | 57 | 57 | 57 |
| 33 | .e.e. | 93 | 3 22 | 222 | 32 32 | 322 | 323 |
| 30 | 7 E | | 36 | : : 80 60 : FT FT | 64 4 | 4 43 8 | 44 45 |

ALIGNMENTS

| н | |
|--------|--------|
| RESULT | A72207 |

proteinase activity modulator HflK - Thermotoga maritima (strain MSB8) ftBH

C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: A72207 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hick Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, I

Nature 399, 323-329, 1999
ArItle: Bvidence for lateral gene transfer between Archaea and Bacteria from genome s Aritle: Bvidence for lateral gene transfer between Archaea and Bacteria from genome s Argeference number: A72207
A,Refatus: preliminary
A,Rotatus: preliminary
A,Rotatus: DNA
A,Rosaiduss: 1-308 <ARN>
A,Cross-references: GB:AR001819; GB:AR000512; NID:g4982396; PIDN:AAD36885.1; PID:g4982

C, Genetics

A;Gene: TM1822 C;Superfamily: erythrocyte band 7 integral membrane protein

Gaps .; 0 Score 37; DB 2; Length 308; Pred. No. 10; 1; Mismatches 1; Indels 66.1%; 75.0%; Query Match
Best Local Similarity 75.0
Matches 6, Conservative

ö

3 WPXGMHY 10 ||| |:|| 41 VVPSGIHY 48 ð 셤

carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N3

C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001
R;Ruroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Og ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
A;Tile: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1057 <KUR>
A;Coss-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149
A;Experimental source: strain N315

A;Gene: pyrAB C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; bioti

Gaps

ö

```
AjExperimental gource: gtrain 9asc
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neto, B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A;Authors: Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fro
J.D.; Junquelra, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Lai
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YBL011w homolog YKR067w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C;Accession: S38143
R;van Vliet-Reedijk, J.C.; Planta, R.J.
R;van Vliet-Reedijk, J.C.; Planta, R.J.
A;Accession: S38130
A;Accession: S38143
A;Molecule type: DNA
A;Residues: 1-743 < VANA
A;Gross-references: EMBL: Z28292; NID: 9486536; PIDN: CAA82146.1; PID: 9486537; MIPS: YKR06
A;Roperimental source: strain S288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: D82618
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D82618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
Residues: 1-156 <SIM>
A;Cross-references: GB:AE004014; GB:AE003849; NID:g9107044; PIDN:AAR84752.1; GSPDB:GNO
         A;Accession: S69046
A;Molecule type: DNA
A;Realdues: 1-460 <HAL>
A;Cossidues: 1-460 <HAL>
C;Genetics:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C,Species: Xylella fastidiosa
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                 A,Map position: 16L
C,Superfamily: Saccharomyces cerevisiae transcription modulator WTM1
                                                                                                                                                                                                                                                                                                                                      Query Match 64.3%; Score 36; DB 2; Length 460; Best Local Similarity 62.5%; Pred. No. 25; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 64.3%; Score 36; DB Local Similarity 75.0%; Pred. No. 43; nee 6; Conservative 1; Mismatches
                                                                                                                                                                                A,Gene: SGD:UMB1
A,Cross-references: SGD:S0006060; MIPS:YPL139c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Map position: 11R
C, Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: SGD:S0001775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 | | | : | |
294 VVPCGLHY 301
A, Reference number: 869040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|| |:||
85 IVPLGLHY 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 WPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SGD: GPT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                    V1 protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Fitle: The nucleotide sequence of the infectious cloned DNA component of tobacco yellc
A;Reference number: A42452; MUID:92188538; PMID:1546458
A;Accession: A42452
A;Accession: A42452
A;Residues: 1-102 cMOR>
A;Residues: 1-102 cMOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Hall, J.; Defaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K. submitted to the EMBL Data Library, December 1995
A; Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein alr1563 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-52 <KUR>
A;Coss-references: GB:BA000019; PIDN:BAB77929.1; PID:g17135383; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein YPL139c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 17-Mar-2000
C;Accession: S69046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                             Score 37; DB 2; Length 1057;
Pred. No. 39;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 64.3%; Score 36; DB 2; Length 252; Best Local Similarity 50.0%; Pred. No. 13; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.3%; Score 36; DB 2; Length 102, 60.0%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                             66.1%;
60.0%;
   Ouery Match
Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                       190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 EMIVPAGLHF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||| |::||
7 OVVPSGINYS 16
                                                                                                                                                                2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetica:
A;Gene: alr1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $69046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                ઠે
                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

ö

Gaps

```
TSIB.1 protein - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: GB6430
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alone Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A.; Li, Y.; Lin, X.; Liu, X.; Liu, Z.A.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rocney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rocney, T.; Rowley, D.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor Ker, M.; Wu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Saquence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G86430
A;Accession: G86430
A;Accession: G86430
A;Accession: G86430
A;Accession: G86430
A;Residues: J-510 cSTO>
A;Residues: J-510 cSTO>
A;Residues: J-510 cSTO>
A;Residues: J-510 cSTO>
A;Residues: GB:AR005172; NID:94587512; PIDN:AAD25743.1; GSPDB:GN00141
                                                                                                                                                                                                                                      C;Accession: T24111
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z18842
A;Reference number: Z18842
A;Accession: T24111
A;Reterence preliminary; translated from GB/EMBL/DDBJ
A;Reterences: EMBL: Z81109; PIDN: CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A;Residues: 1-425 <WIL>
A;Residues: CESP:R10D12.10
A;Reperimental source: clone R10D12
C;Genet.cs:
A;Gene: CESP:R10D12.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Methanobacterium thermoautotrophicum
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Feb-2003
C; Accession: G69117
                                                                                                                                                  hypothetical protein R10D12.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T24111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diphthine synthase - Methanobacterium thermoautotrophicum (strain Delta H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 35; DB 2; Length 510;
60.0%; Pred. No. 45;
ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.5%; Score 35; DB 2; Length 425; 50.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics:
A,Map position: 1
C,Superfamily: hexose phosphate transport protein uhpT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Map position: 5
A,Introns: 23/3; 56/3; 113/3; 257/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5, Conservative
      219 REVVESGLHES 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 EQIVPGGLQY 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 REVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 BEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 BEVKPPGIHF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
G86430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G69117
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GMP synthetage, subunit B - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: H69194
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
C;Otu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
J; Sarchurch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J; Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUD:98037514; PMID:9371463
A;Attus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-311 < MTH>
A;Residues: 1-311 < MTH>
A;Residues: 1-311 < MTH>
A;Residues: 1-311 < MTH>
A;Residues: 1-311 emth>
A;Residues: 1-311 < MTH>
A;Residues: 1-311 surfain Delta H
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.P.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., M.A.; da Silva, A.M.; Silva Jr., M.A.; da Silva, A.M.; Freference mumber: A59328
A;Contents: annotation
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RiOhme-Takagi, M.; Shinshi, H.
Dlant Cell.7, 173-182, 1995
A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene responsi
A;Reference number: Z14671; MUID:95276459; PMID:7756828
                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA binding protein EREBP-2 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                    62.5%; Score 35; DB 2; Length 156; 55.6%; Pred. No. 13; 1.1ve 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 2; Length 233;
Pred. No. 19;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 35; DB 2; Length 311; 63.6%; Pred. No. 27; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : ||| | ||
90 QAVVPKGRHY 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||::||:|
119 BEILPQGVH 127
                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                           1 BEVVPXGMH
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Accession: T02590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: MTH710
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

Gaps

ö

2; Indels

ö

Gaps

Length 350; 3; Indels

```
C;Species: Streptomyces coelicolor
C;Dates 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35025
R;Seeger, S:; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.355 <SER>
A;Residues: 1.355 <SER>
A;Cross-references: EMBL:AL079355; PIDN:CAB45581.1; GSPDB:GN00070; SCOEDB:SC4C6.17c
C;Genetics:
A;Rxperimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC4C6.17c
A, Experimental source: strain R1
C;Genetics:
A,Genee: DRO/1
A,Map position: 1
C;Superfamily: 3-dehydroquinate synthase; 3-dehydroquinate synthase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 355;
                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                       Score 34; DB 2
Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.7%; Score 34; DB 71.4%; Pred. No. 49; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable DNA ligase - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: December 22, 2003, 17:44:57 Job time : 9.06667 secs
                                                                                                                                                                                                                                                       Query Match 60.7%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 71.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 KAVAYGMHYA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 IPPGMHY 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S. Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-264 cMTH>
A;Residues: 1-264 cMTH>
A;Residues: 1-264 cMTH>
A;Residues: BNA
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: C7558
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ms.; Science 286, 1571-1577, 1999
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-dehydroquinate synthase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75478
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE001932; GB:AE000513; NID:g6458481; PIDN:AAF10353.1; PID:g645848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: DR0271
A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR0271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.7%; Score 34; DB 2; Length 279; llarity 75.0%; Pred. No. 38; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.7%; Score 34; DB 2; Best Local Similarity 62.5%; Pred. No. 35; Matches 5; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| |:|:
235 VVPAGLHF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 VPLGRHYS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: B75478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

ö

Gaps

ö

Indels

٠,

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                       OM protein - protein search, using sw model
```

December 22, 2003, 16:43:51; Search time 4.6 Seconds Run on:

(without alignments) 112.455 Million cell updates/sec

US-09-909-164-11 56

Perfect score:

1 BEVVPXGMHYS 11 BLOSUM62 Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | ption | fusobacteri | vibrio para | staphylococ | staphylococ | tobacco yel | Baccharomyc | Baccharomyc | mesocricetu | methanobact | yarrowia li | vibrio para | desulfovibr | bacillus su | caenorhabdi | bacteriopha | bos taurus | clostridium | chlorella v | rattus norv | homo sapien | mus musculu | brachydanio | xenopus lae | gallus gall | xenopus lae | gallus gall | homo sapien | homo sapien | mus musculu | rattus norv | azotobacter | bacillus an | drosophila |
|-----------|----------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|
| | Description | Q8rg86 | 087qx9 | Q99ur5 | P58940 | P31619 | 003010 | P36148 | 035586 | 026806 | 099158 | P46231 | P13065 | P49850 | P34335 | P13390 | P08858 | 097166 | P56351 | 004827 | P30279 | P30280 | 090459 | P50755 | P49706 | P53782 | P55169 | P30281 | P24385 | P25322 | P39948 | P40595 | P19887 | Q9vwp4 |
| SUMMAKIES | ΩI | CARB FUSIN | AROA VIBPA | CARB STAAM | CARB_STAAW | Y11K_TYDVA | UME1_YEAST | YK47_YEAST | IDI1 MESAU | GAAB_METTH | SLS1_YARLI | /L15_VIBPA | PHSL_DESBA | MUTL_BACSU | KPBA_CAEEL | /LTF_BPT5 | TKNK_BOVIN | RS2_CLOAB | RR2_CHLVU | CGDZ_RAT | CGD2_HUMAN | CGD2_MOUSE | CGD1_BRARE | CGD1_XENLA | GD2_CHICK | CGD2_XENLA | CGD1_CHICK | CGD3_HUMAN | CGD1_HUMAN | CGD1_MOUSE | CGD1_RAT | HYPE_AZOVI | T2BA_BACAR | SUOX_DROME |
| | DB | - | - | | | _ | - | H | -1 | - | - | | - | - | - | H | - -1 | - - | - - | | - | | | | | | | | - | | - ٦ | - - | Н | |
| | Length | 1058 | 426 | 1057 | 1057 | 102 | 460 | 743 | 227 | 308 | 426 | 441 | 513 | 627 | 1188 | 1396 | 126 | 233 | 267 | 288 | 289 | 289 | 291 | 291 | 291 | 291 | 292 | 292 | 295 | 295 | 295 | 341 | 353 | . 573 |
| * | Query Match | 67.9 | 66.1 | 66.1 | 66.1 | 64.3 | 64.3 | 64.3 | 62.5 | 62.5 | | | | | 58.9 | 58.9 | 57.1 | 57.1 | 57.1 | 57.1 | 57.1 | | | | | 57.1 | 57.1 | • | • | | • | ٠ | 57.1 | 57.1 |
| | Score | 38 | 37 | 37 | 37 | 36 | 36 | 36 | 35 | 35 | 34 | 33 | 33 | 33 | 33 | 33 | 32 | | 32 | | | | | | | | | 32 | 32 | 32 | 32 | 32 | 32 | 32 |
| | Result No. | - | 7 | ж \ | 4 | S | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 50 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 53 | 30 | 31 | 32 | 33 |

PF00289; CPSase L Chain; 2. PF02786; CPSase L D2; 2. PF02787; CPSase L D3; 1.

Pfam; Pfam;

| Q89996 buchnera ap P3784 saccharomyc O74377 schizosacch Q9kv29 vibrio chol P15822 homo sapien P20273 homo sapien P20273 homo sapien P27280 chimpanzee P9788 rattus norv Q58349 methanococc P10941 cryphonectr O28354 archaeoglob P52210 ovis aries |
|--|
| MOLB BUCBP SCT1 YEAGT SULH-SCHPO REDC VIBCH CD22 HUMAN CD22 HUMAN REV SIVCZ S205 RAT Y939 METJA YHA1 CRYPA RL3 ARCFU |
| ананананана |
| 578 759 877 1401 2717 847 130 276 319 331 |
| 20000000000000000000000000000000000000 |
| 32 32 32 31 31 31 31 31 |
| ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ |

ALIGNMENTS

```
REPURINGE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 25586;

MEDLING=21886394; PubMed=11889109;

RA Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Battacharyya A., Battman A., Gardner W., Grechkin G., Zhu L.,

RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman B., Bernal A.,

RA Larsen N., D'Souva M., Walunas T., Pusch G., Haselkorn R.,

RA Learen N., D'Souva M., Overbeek R.;

RA Learen N., D'Souva M., Overbeek R.;

RA Learen M., Kyrpides N., Overbeek R.;

RA Learen M., Kyrpides N., Overbeek R.;

RA Learen M., Ryrpides N., Overbeek R.;

RA Learen M., Ryrpides V., Overbeek R.;

RA Learen M., Ryrpides V., Overbeek R.;

RA Learen M., Syrpides V., Overbeek R.;

L. CAPLANTI ACTIVITY: 2 ATP + L-Glutamine + CO(2) + H(2)O = 2 ADP + Dhosphate + L-Glutamate + carbamoyl phosphate.

C. I. COPACTOR: Binds 3 manganese ions per subunit (By similarity).

C. I. PATHWAY: Arginine biosynthesis.

C. I. PATHWAY: Pyrimidine biosynthesis, first step.

C. I. PATHWAY: Pyrimidine biosynthesis, the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by similarity).

C. I. SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.lsb-sib.ch/announce/or send an email to license@ib.ch).
                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamcyl-phosphate synthase large chain (RC 6.3.5.5) (Carbamcyl-phosphate synthetase ammonia chain)
CARB OR FN0422.
CARB OR FN0422.
FURObacterium nucleatum (subsp. nucleatum).
Bacteria; Pusobacteria; Fusobacterales; Fusobacteriacee;
                                              PRT; 1058 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE010554; AAL94625.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 01210; -; 1.
InterPro; IPR006275; CarA L glu.
InterPro; IPR005483; CPase L.
InterPro; IPR005499; CPase L.
InterPro; IPR005480; CPase L. D3.
InterPro; IPR005481; CPase L. D3.
InterPro; IPR005481; CPase L. D3.
InterPro; IPR004362; MGS_IIke.
                                              STANDARD;
                                                                                                                                                                                                                                                                                           NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                      Pusobacterium
                                            CARB FUSIN
RESULT 1
CARB_FUSNN
```

```
Best Loc
Matches
8 2 2 B
                                                                                                                              셤
                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=RIMD 2210633 / Serotype 03:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iljima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Yubrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (APSPS), AROA OR VP1020.
                 TIGREPARS; TIGROUSES; CERRAGEII lrg; 1.
PROSITE; PSOURGE; CPSASE 1; 2.
RNOSITE; PSOURGE; CPSASE 2; 2.
Arginine biosynthesis; Pytrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome.
DOMAIN 402 546 GARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                     ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
AMANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
AMANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                 DB 1; Length 1058;
                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBUNIT: Monomer (By similarity).
-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                 Score 38; DB 1
Pred. No. 10;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP005076; BAC59283.1; -.
                                                                                                                                                                                                                                                                67.9%;
                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                |:|| |::||
190 EIVPNGLNYS 199
             PRINTS; PR00098; CPSASE
                                                                                                                                                                                                                                                                                                                  2 EVVPXGMHYS 11
                                                                                                                                                      153 210
302 352
284 284
298 298
300 300
820 820
832 83;
Pfam; PF02142; MGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00210; -; 1
                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sixth step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                    VIBPA
                                                                                                                                                                                                                              METAL
SEQUENCE
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                REPEAT
REPEAT
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                     AROA VIB
Q87QX9;
                                                                                                                                                                                           METAL
METAL
                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                      AROA VIBPA
                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                         셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
STRAIN=MISO, ARCC 700699, and Nils;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
MIDLINE=21311952; PubMed=11418146;
Minch M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Kanda M., Maruyama A., Murakami H., Hosoyama A., Mizutani H., Maruyama A., Mizutani H., Hosoyama A., Mizutani Ui Y., Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kaito C., Kannehisa M., Vameshita A., Oshima K., Puruya K., Yoshino C., Shiba "Mattori M., Ogasawara N., Hayashi H., Hiramatau K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FRB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last sequence update)
Carbamoyl-phosphate synthase large chain (RC 6.3.5.5) (Carbamoyl-phosphate synthase amonia chain).
CARB OR PYRAB OR SAV1203 OR SA1046.
Staphylococcus aureus (strain Muso) / ATCC 700699), and Staphylococcus aureus (strain Muso).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
PROSITE; PS008B5; EPSP_SYNTHASE_2; 1.
Aromatic amino acid blosynthesis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46094 MM; 373D39CC5BA1F70F CRC64;
                                                                                                                                                                                                                  ö
                                                                                                                                                66.1%; Score 37; DB 1; Length 426; 60.0%; Pred. No. 6.3;
                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1057 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P00968; ICSO.
HAWAP, MF 01210; -; 1.
InterPro; IPR00545; CarA L_glu.
InterPro; IPR005483; CPase L.
InterPro; IPR005489; CPase L.
InterPro; IPR005480; CPase L.
InterPro; IPR005480; CPase L.
InterPro; IPR005481; CPase L.
InterPro; IPR005481; MGS like.
Pfam; PP00289; CPSase L.Chain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP003361; BAB57365.1; -. EMBL; AP003132; BAB42298.1; -. PIR; F89892; F89892.
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                          223 BFVIPAGOHY 232
                                                                                                                                                                                                                                                                        1 REVVPXGMHY 10
                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARB STAAM
ID CARB STAAM
AC Q99UR5;
                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aureus.";
```

Ę

us-09-909-164-11.rsp

```
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                      Arginine blosynthesis; Primidine blosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 1; Length 1057; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1057 AA; 117185 MW; D8E3B09F9BC6F152 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                             PRINTS; PRO0098; CPSASE.
TIGRAMB; TIGRO1369; CPSASE11_lrg; 1.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE_2; 2.
                                      HANARA MF 01210; .; 1.
InterPro; IPR005475; Cara L glu.
InterPro; IPR005479; CPase L. D.
InterPro; IPR005480; CPase L. D.
InterPro; IPR005480; CPase L. D.
InterPro; IPR005480; CPase L. D.
InterPro; IPR005481; CPase L. D.
InterPro; IPR005481; CPase L. D.
Fam; PP00289; CPSsse L. Chain; 2.
Fam; PP02786; CPSsse L. Chain; 2.
Fam; PP02787; CPSsse L. D.3; 1.
Pfam; PP02142; MGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92188538; PubMed=1546458;
                          AP004825; BAB94951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-OCT-1993 (Rel. 27, Last ann
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                        929
1057
546
1057
                                                                                                                                                                                                                                                                                                                                                                                   401
546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y11K TYDVA
ID Y11K TYD
AC P31619;
T 01-,TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
NP BIND
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R Pfam; PF02786; CPSase_L_D3; 1.

Pfam; PF02787; CPSase_L_D3; 1.

R Pfam; PF02182; MGS; 1.

R R Pfam; PF02182; MGS; 1.

R R Pfam; PF00198; CPSASE

R TIGRFAMB; TIGR01369; CPSASE 1; 2.

R PROSITE; PS00866; CPSASE 1; 2.

R PROSITE; PS00866; CPSASE 2; 2.

M Arginine biosynthesis; Primidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Ligase; Repeat; M ATP-binding; Manganese; Complete proteome.

CARBOXPHOSPHATE SYNTHETIC DOMAIN.

T DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

T DOMAIN 930 1057 ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=22040717; PubMed=12044378;

MEDLINE=22040717; PubMed=12044378;

Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagan Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamanco K., Hiramatan K.;

"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
phosphate synthetes annonia chain (EC 6.3.5.5) (Carbamoyl-CARB OR PYRAB OR MW1086.
                                                                                                                                                                                                                                                                                                                                        MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.1%; Score 37; DB 1; Length 1057; 60.0%; Pred. No. 16; 2; Indels tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1057 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        117171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                             547 105:
153 21:
302 35:
284 28
298 29
300 30
820 82
832 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARB STAAW
P58940;
                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
SEQUENCE
                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARB STAAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DARAGE STATE OF THE SOLUTION O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

ö

Gaps

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                    Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nucleotide sequence of the infectious cloned DNA component tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotylednous plants.";
virology 187:633-642(1992).
Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
```

SANA

à 셤

```
STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YK47 YEAST
ID YK47 YEAST
AC P36148;
                                                                                                                                                                                                                                                      REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKR067W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CETRAIN=S288C / AB972;

WEDLINE=97313271; PubMed=9169875;

WEDLINE=97313271; PubMed=9169875;

WEDLINE=97313271; PubMed=9169875;

Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Araujo R., Aparicio A., Burnerla M., Carpenter J., Cherry J.M., Ansorge M.D., Botstein D., Bowman S., Burkener M., Cherry J.M., Botstein D., Bowman R., DiRaolo E., Duncia R.W., Allent H., Hillier L., Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Amarathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., Amarathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., Amarathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., Amarathe R., Messenguy F., Mewes H.-W., Scharfe M., Schramm S., Schramm S., Schramm S., Schramm S., Schramm S., Schramm S., Wedler R., Wedler R., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett B., Ander M., Albert B., Schramm S., Schramm S., Wedler E., Wedler H., Winnett B., Ander M., Alber B., Schramm S., Wedler E., Wedler H., Winnett B., The nucleotide sequence of saccharomyces cerevisiae chromosome XVI.";

Nather 387.103-105(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                         ö
                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: TRANSCRIPTIONAL MODULATOR WITH ROLES IN MEIOTIC REGULATION AND SILENCING. NEGATIVE REGULATOR OF MEIOSIS. -!- SIMILARITY: CONtains 4 WD repeats. -!- SIMILARITY: STRONG, TO YEAST WIMI AND WIM2.
                                                                                                                Score 36; DB 1; Length 102;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                  InterPro, IPR002621; Gemini mov.
Pfam, PR01708; Gemini mov.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIEOAF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             , Last sequence update)
                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Meiosis negative regulator UME1. UME1 OR WIM3 OR YPL139C OR LPI7C
                                                                                                                                                                                                                                                                                                                                UME1 YEAST STANDARD; 1003010; P87330; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last seq. 28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U10280; AAB40937.1; -.
                                                                                                                64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U43703; AAB68221.1; -. PIR; S69046; S69046.
TRANSFAC; T04309; -. SGD; SO006060; UMB1.
                                                                                                                                   Local Similarity 60.0
les 6; Conservative
                                                                                                                                                                                                                     2 EVVPXGMHYS 11
PIR; A42452; A42452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A364A;
                                                                                                                    Query Match
                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                               RESULT 6
```

THE PROPERTY OF COURSE BY A PRANCE BY A PRANCE OF COURSE BY A PRANCE OF COURSE BY A PRANCE BY A PRANCE

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO, GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0004366; F:glycerol---phosphate O-acyltransferase acti. . .; IDA.
GO; GO:0008654; P:phospholipid biosynthesis; IDA.
InterPro; IPRO2123; Acyltransferase.
Ffam; PPO1553; Acyltransferase; 1.
SWART; SM00563; Plsc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van Viiet-Reedijk J.C., Planta R.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
GO; GO:0005634; C:nucleus; IDA.

R GO; GO:0003714; F:transcription co-repressor activity; IDA.

GO; GO:0003714; F:transcription of meiosis; IGI.

R InterPro; IPR001680; WD40.

R PÉRM; PR00400; WD40; 3.

R PROSITE; PR500320; WD40; 4.

R PROSITE; PR50062; WD_REPEATS_1; FALSE NEG.

R PROSITE; PR50082; WD_REPEATS_2; PALSE NEG.

R PROSITE; PR50082; WD_REPEATS_REGION; FALSE NEG.

R TRANSCRIPCION requisition; Meiosis; Repeat; WD repeat.

R REPEAT 233 271 WD 2.

R REPEAT 339 379 WD 3.

R REPEAT 411 451 WD 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-ZUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCP1-MET1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Length 743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 1; Length 460;
Pred. No. 11;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 85 POTENTIAL.
502 524 POTENTIAL.
539 555 POTENTIAL.
743 AA; 83644 MW; 84B9946ES6B82F15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            AA6F60448B7BCBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         743 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.3%; Score 36; DB 75.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                            460 AA; 51022 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z28292; CAA82146.1; -. PIR; S38143; S38143.
SGD; S0001775; GPT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 62.5
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 IVPLGLHY 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 WPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
```

RESULT

ઠે g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-Debla H.

WEDINE-Debla K.

WEDINE H.

WEDIN
                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
GMP synthase (glutamine-hydrolyzing) subunit B (BC 6.3.5.2) (GMP
                                                                                                                                                                                                                                                   GÜAAB OR MTH710.
Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MP_00345; -; 1.
InterPro; IPR001674; GMP synt_C.
Ema; PR00958; GMP synt_C.
FIGRPAMs; TIGR00864; guaA. Cterm; 1.
Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 35; DB 1; Length 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 184 GMP-BINDING (BY SIMILARITY).
29 35 ATP (BY SIMILARITY).
308 AA; 34403 MW; P2DCP6ED202CAECI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YARLI SIMULE SIM
   308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000850; AAB85215.1; ALT_INIT.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 63.6
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 REVVESGLHES 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 REVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P04079; 1GPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ligase; GMP blosynu
Complete proteome.
GAAB METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLS1_YARLI
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 È
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                30-MAY.2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (IRel. 42, Last annotation update)
11-Sepentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.2) (IPP isomerase 1) (Isopentenyl pyrophosphate isomerase 1) (IPPII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=97373600; PubMed=9228075;

Paton V.G., Shackelford J.B., Krisans S.K.;

"Cloning and subcellular localization of hamster and rat isopentenyl diphosphate dimethylallyl diphosphate isomerase. A PTS1 motif targets the enzyme to peroxisomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 272:18945-18950(1997).
-!- FUNCTION: CATALYZES THE 1,3-ALLYLIC REARRANGEMENT OF THE HOMOALLYLIC SUBSTRATE ISOPENTENTE, (IPP) TO ITS HIGHLY ELECTROPHILIC ALLYLIC ISOMER, DIMETHYLALLY DIPHOSPHATE (DMAPP).
-!- CATALYTIC ACTIVITY: ISOPENTENY diphosphate = dimethylallyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isoprene biosynthesis; Sterol biosynthesis; Isomerase; Peroxisome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
-!- PATHWAY: ISOPRENOID BIOSYNTHETIC PATHWAY WHOSE END PRODUCTS
INCLUDE DOLICHOLS, VITAMINS A, D, E, AND K, STEROID HORMONES,
CAROTENOIDS BILE ACIDS AND CHOLESTEROL.
-!- SUBCELLULAR LOCATION: Peroxisomal.
-!- SIMILARITY: Belongs to the IPP isomerase type 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 1; Length 227; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 BY SIMILARITY.
148 BY SIMILARITY.
NTCROBODY TARGETING SIGNAL.
26317 MW; P500A6586385E803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cholesterol biosynthesis;
                                                                                                                                                                                                                                                                                         227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF003836; AAC53283.1; -. InterPro; IRRO02667; IPP isomerase. InterPro; IRR000866; NUDIX_hydrolase. Pfam; PF00293; NUDIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom, PD004109, IPP isomerase; 1. Carotenoid biosynthesIs; Cholestero
                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
15-SEP-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 EEVDPNEMHY 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMHY 10
                                                                            ||| |:||
294 VVPCGLHY 301
                                  3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
148 1
225 2
227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diphosphate.
                                                                                                                                                                                                                                                                                         IDI1 MESAU
035586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

PACTOR OF THE PROPERTY OF THE

ö

Gaps

ö

3, Indele

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

GAAB_METTH RESULT 9

ద ઠે

```
Bacteriol. 176:4219-4225(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 BTWPTFIHYN 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 BEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=899;
                                                                                                                                                                                                                                                                                             Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHSL DESBA
P13065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          baculatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CE REPARE TO SERVICE S
                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                        SEQUENCE FROM N.A.

C STRAIN=ATCC 20460 / W29;

X MEDLINE=96216076; PubMed=8662639;

Boistrame A., Beckerich J.-M., Gaillardin C.;

Boistrame A., Beckerich J.-M., Gaillardin C.;

"Sl81p, an endoplasmic reticulum component, is involved in the protein translocation process in the yeast Yarrowia lipolytica.";

J Biol. Chem. 271:11668-11675(1996).

INTERACT DIRECTLY WITH TRANSLOCATING POLYPEPTIDES TO FACILITATE TRANSFER AND/OR HELP THEIR POLDING IN THE ER. IT IS NOT REQUIRED FOR VIABILITY BUT IS ESSENTIAL FOR OPTIMAL GROWTH AT ELEVATED TEMPERATURES.

C SLEVATED TEMPERATURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEST PROTEIN.
PREVENT SECRETION PROM ER (POTENTIAL)
, 0ACD/2E117540B8E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.7%; Score 34; DB 1; Length 426; 44.4%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Moty, a component of the sodium-type flagellar motor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical protein VP2115 (ORF3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 AA
    Saccharomycetales, Dipodascaceae, Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94292449; PubMed=8021208; McCarter L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000886; ER target. PROSITE; PS00014; ER TARGET; 1. Endoplasmic reticulum; Signal. SIGNAL 17 PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 AA; 47201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z50154; CAA90516.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-140 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio parahaemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::|:| |:|
52 DQVIPAGLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BB22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YL15 VIBPA
P46231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
Periplasmic [NiFeSe] hydrogenase large subunit (BC 1.12.99.6) (NiFeSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99906038; PubMed=10378275;
Garcill B., Vernede X., Hatchikian B.C., Volbeda A., Frey M.,
Pontecilla-Camps J.C.;
Removal of the bridging ligand atom at the Ni-Fe active site of
[NiFe] hydrogenase upon reduction with H2, as revealed by X-ray
structure analysis at 1.4-A resolution.";
Structure 7:557-566(1999).
-I- CATALYTIC ACTIVITY: H(2) + acceptor = 2 H(+) + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hydrogenlyase large cháin).
Besulfowiczobłum baculatus).
Bacteria, Proteobacteria, Deltaproteobacteria, Desulfowibrionales;
Desulfomicrobiaceae; Desulfomiczobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-88058744; PubMed=1316183; Menon N.K., Peck H.D. Jr., 16 Gall J., Przybyla A.E.; Caloning and sequencing of the genes encoding the large and small subunits of the periplasmic (NiPeSe) hydrogenase of Desulfovibrio

    BUBCELLULAR LOCATION: Integral membrane protein (Potential).
    BIMILARITY: STRONG, TO H. INPLUENZAE H10325.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 1; Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451969FB307B4D46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Menon N.K., Pect H.D. Jr., le Gall J., Przybyla A.E.; J. Bacteriol. 170:4429-4429(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 43;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol, 169:5401-5407(1987)
                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP005080; BAC60378.1; -. EMBL; U06949; AAA21571.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45961 MW;
```

```
SECURENCE FROM N.A.
STRAIN=168;
MEDLINE=96349107; PubMed=8760914;
Ginetti F., Perego M., Albertini A.M., Galizzi A.;
"Bacillus subtlils mutS mutL operon: identification, nucleotide sequence and mutagenesis.";
Microbiology 142:2021-2029(1996).
                                                                                                                                                                                                                                                                                                                                                                                                         58.9%; Score 33; DB 1; Length 513; 71.4%; Pred. No. 50; 1; Mismatches 1; Indels ive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                        56683 MW; AC8285A6F80576FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA mismatch repair protein muth.
                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
 297 PGGLHYS 303
                                                                                                                                                                                                                                                                                                                                                                    492 4
493 4
513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTL.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
 RESULT 13
MUTL BACSU
ID MUTL BACSU
AC P49850;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
HELIX
STRAND
STRAND
TURN
STRAND
STRAND
STRAND
STRAND
TURN
STRAND
TURN
STRAND
                                                                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                                                                                                                                                                                                                                                    STRAND
                                                                                                                                                                                                                                                                                                  TURN
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                 HBL IX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                             | Reward | R
                                                 ⋖
                     ligands.
SUBUNIT: Heterodimer of a large and a small subunit.
SUBCELLULAR LOCATION: Periplasmic.
MISCELLULAR LOCATION: PERHAPS THE LEADER OF THE SMALL SUBUNIT SERVES AS
MISCELLANBOUR: VEHICLE FOR BOTH SUBUNITS.
SIMILARITY: BELONGS TO THE [NIFE]/[NIFESE] HYDROGENASE LARGE
SUBUNIT FAMILY.
COFACTOR: Nickel, 2 irons and selenocysteine. Iron 1 has three cyanide and carbon monoxide ligands. Iron 2 has three water
                                                                                                                                                                                                                                                               ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                              HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
TURN
HELIX
TURN
HELIX
TURN
HELIX
STRAND
TURN
HELIX
STRAND
HELIX
STRAND
STRAND
STRAND
STRAND
STRAND
STRAND
```

Gaps

;

PRT; 1188 AA.

STANDARD;

CARRI

RESULT'14 KPBA CABBL

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                        RA Kunst F. Ogsaswara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Colladwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Erlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Mizuno M., Moeslt D., Nakai S., Nuoback M.,
RA Medina N., Mellado R.P., Mizuno M., Moeslt D., Nakai S., Nuoback M.,
RA Medina N., Mellado R.P., Mizuno M., Moeslt D., Nakai S., Nuoback M.,
RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan B., Schoeis B., Roche B., Rose M., Sator T.,
RA Sator J., Sarons B., Polieich S., Schroeter R., Vassarotti A.,
RA Sorokin A., Tacconi B., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Seror S.J., Serror P., Shin B.S.,
RA Vasidu K., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT "The Complete genome sequence of the Gram-positive was and target supplicit with the supplicit of the Gram-positive was and target supplicit with the supplicit of the Gram-positive was and target supplicit with the supplicit of the Gram-positive was and target supplicit with the supplicit of the Gram-positive was and target supplicit with the supplicit of the Gram-positive was and targe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).

-! FUNCTION: THIS RECOTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN DNA. IT IS REQUIRED FOR DAM-DEPENDENT METHYL-DIRECTED DNA MISMATCH REPAIR. MAY ACT AS A "WOLECULAR MATCHANKER", A PROTEIN THAT PROMOTES THE FORMATION OF A STABLE COMPLEX BETWEEN TWO OR MORE DNA-BINDING PROTEINS IN AN ATP-DEPENDENT MANNER WITHOUT ITSELF BEING PART OF A FINAL REFECTOR COMPLEX (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.9%; Score 33; DB 1; Length 627; 54.5%; Pred. No. 62; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  068A0509CC265343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00058; DNA MISWATCH REPAIR_1; 1.
DNA repair; Complete proteome.
SEQUENCE 627 AA; 70431 MW; 068A0509CC265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Subtitist; BG11402; mutt.
HAWAP; MF 00149; -; 1.
InterPro; IPR003594; ATPbind ATPase.
Ptenry: IPR020399; DNA_mis_repair.
Pten; PF01119; DNA_mis_repair.
Pfam; PF02518; HATPase_c; 1.
                               MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U27343; AAB19236.1; -. EMBL; Z99112; CAB13578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00387; HATPase c; 1
TIGRFAMs; TIGR00585; mutl; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A69663; A69663.
HSSP; P23367; 1BKN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable phosphorylase B kinase alpha regulatory chain (Phosphorylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coulson A.,
                                                                                                                                                                                                                       Bukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                               PROJUCE FOR MAN AND MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein, Glycogen metabolism, Calmodulin-binding.
SEQUENCE 1188 AA; 135558 MW; DE9BBB75F3603863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.9%; Score 33; DB 1; Length 1188; 54.5%; Pred. No. 1.2e+02; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLTF BFT5

VLTF BFT5

AC P133\overline{0}0, O48502;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FBB-1996 (Rel. 33, Last sequence update)

DT 01-RB-1996 (Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L15188; AAA27954.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormPep; C14B9.8; CE26870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 54.5
nes 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              950 EEYAEDGIHYS 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 BEVVPXGMHYS 11
                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                           kinase alpha subunit).
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                         C14B9.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

ö

Gaps

ö

6; Conservative

Matches

ઠે

Local Similarity

```
DB L-shaped tail fiber protein (LTF protein).

OS Macteriophage T5.

OC Virtues; daDMA viruses, no RNA stage; Caudovirales; Siphoviridae;

OC T5-11ke viruses

OC T6-11ke viruses

OC T6-1
```

Search completed: December 22, 2003, 17:42:26 Job time : 4.6 secs

2 EVVPXGMHYS 11 ::| | | | | 1360 KTIPAGDHYS 1369

ઠે

```
Q8k289 mus musculu Q8cpj4 staphylococ Q8x22 thermocoga Q9hlh8 thermochococ Q46486 corynebacte Q8ywp1 anabaena sp Q9xx4 pisum sativ Q57489 bacteroides Q9pc35 xylella fas Q9pc35 xylella fas Q9lw50 nicotiana t Q9lw50 nicotian
                                                                                                                                                                  December 22, 2003, 17:27:26; Search time 25.2 Seconds (without alignments) 112.642 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPTREMBL 23:*

1: sp archea:*
2: sp bacteria:*
3: sp fung1:*
4: sp luman:*
1: sp muman:*
5: sp mhc:*
8p phage:*
8p phage:*
8p phage:*
8p codent:*
8p virv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8K289
Q8CPJ4
Q9K2E2
Q9HLH8
Q8DIH0
Q46486
Q8YWP1
Q9AVK4
Q57489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PC35
Q40479
Q9LW50
Q38317
Q9XVK4
                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9006
                                                                                                                                                                                                                                                                                                     US-09-909-164-11
56
1 REVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
```

| O27902 methanobact O97xn9 deinococcus O98Mus rhizobium 1 O97xw92 deinococcus O97xw92 deinococcus O97xw92 deinococcus O97xw92 deinococcus O97xp1 methanobact O94xp1 methanobact O94yc1 ranid herpe O89xp1 ranid herpe O89xp1 ranid herpe O89xp1 ranid herpe O80xp2 mus musculu O89xp1 ranid herpe O80xp1 ranidatus O91xp1 prototheca O90xp1 ranidatus O91xp1 prototheca O80xp1 ranidatus | PRT; 413 AA. 22, Created) 22, Last sequence update) 23, Last annotation update) 1997856. chence A1987856. the EMBL/GenBank/DDBJ databases. chence A1987878. chence A1, DBJ databases. chence A1, DBJ li, Length 413; 24; Score 41; DB li, Length 413; 64; Pred: No. 5.4; chence A1, DB li, Length 413; chence A1, DB li, | T; 1057 AA. ted) sequence update) annotation update) ge chain. |
|---|--|---|
| 027902 098406 098406 098403 097401 08CAL1 08CAL1 091512 097801 097801 097801 097801 097801 097801 097801 098704 098704 098704 098704 098704 098704 098704 098701 | ALIGNMENTS LRY; PRT; 413 A 11. 22, Created) 12. 22, Last sequence 11. 23, Last sequence 12. 23, Last sequence 13. 24, Last sequence 14. 25, Last sequence 16. 1987856. hordata, Craniata; Ve codentia; Sciurognathi to the EMBL/GenBank/D 195. 1; 10004BB19Rik. 6621 MW; A9B8AlDC70C 6621 WW; A9B8AlDC70C 663. 1; Pred. No. 5.4 1. | PRT; 1057 Created) Last sequenc Last annotat large chain |
| | × 10 10 × 1 1 10 14 15 | O O |
| 106 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | NRY; 11. 22, 11. 22, 12. 23, 13. 24, 14. 25, 15. 26, 16. 26, 17. 28, 17. 28; 17. 28; 17. 28; 17. 28; 17. 28; 17. 28; | 23, 23, 23, thas |
| 264 274 274 274 274 274 274 274 274 274 27 | PRELIMINARY; P) 27-2002 (TYENBLIAL 22, Cre- T-2002 (TYENBLIAL) 23, Last RA-2003 (TYENBLIAL) 23, Last RA-2003 (TYENBLIAL) 23, Last RA-2003 (TYENBLIAL) 23, Last RA-2003 (TYENBLIAL) 23, Last Last took of the control of | MARY, rel. rel. synt |
| 66666666666666666666666666666666666666 | PRELIMIN (TrEMEL: (T | ELLI FELLI FEM FEM TrEM |
| | PRELIMIN 2002 (TrEMBLE 2003 (TrEMBLE CO SYLEMBLE CO SYLEMBLE CO SYLEMBLE CO SYLEMBLE CO SYLEMBLE CO STERMBLE CO ST | EKIPPLGKHYS PRELIMIN 03 (TERMELT 03 (TERMELT -phosphate |
| \$ | | 168 EEIPELGKHY, 74 (2002) 74 (2002) 75 (2003) 76 (2003) 77 (2003) 77 (2003) 77 (2003) 77 (2003) 77 (2003) 77 (2003) 78 (2003) 78 (2003) 78 (2003) |
| 11112222222222222222222222222222222222 | SULT 1 K289 Q8K26 Q8K26 01-OC 01-OC 01-N 01-M SIMIN MARTIN | 11.7 4.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 |
| € | 78 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | RESULT PRESULT 1D CP44 DT 00 DT 00 D |
| | | |

SCARRACO

```
FTRAIN-DSM 1728; MEDLINE-20479972; PubMed=11029001; Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 17; Length 322;
Pred. No. 27;
1; Mismatches 1; Indels
              Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmatacae; Thermoplasma.
NCEL_TaxID=2303;
                                                                                                                                                                                                                                                                                                                            322 AA; 36918 MW; B8C239E71009D167 CRC64;
Glucose-fructose oxidoreductase related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1044 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                         Nature 407:508-513(2000).
EMBL; ALG45063; CAC11395.1; -.
InterPro; IPR000683; GFO_IDH_McA.
Pfam; PF01408; GFO_IDH_MocA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                            Query Match 66.1%;
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||:| |: ||
843 EEVLPNGIGYS 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EBVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 WPDGLHY 73
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            Complete proteome
SEQUENCE 322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (
01-NOV-1996 (
01-MAR-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      046486
046486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8DIH0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99287316; PubMed=10360571;
Nelson K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nelson K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
                                                                                                     Oin 2.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                             ö
                                                                                   STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y.,
Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016746; AAO04476.1; -.
                                                                                                                                                                                                                       Score 39; DB 16; Length 1057;
Pred. No. 38;
2; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 16; Length 308; Pred. No. 26; 1; Mismatches 1; Indels
                                                                                                                                                                           Complete proteome.
SEQUENCE 1057 AA; 117391 MW; 8944D7D8DB1CAE59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease; Complete proteome.
SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9X2E2;
01-NOV-1999 (TrEWBLrel. 12, Created)
01-NOV-1999 (TrEWBLrel. 12, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
FTSH protease activity modulator HFLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
 Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                    308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001107; Band 7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band 7; 1.
PRINTS; PR00721; STOMATIN.
SWART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001819; AAD36885.1; -. TIGR; TM1822; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.1%;
75.0%;
                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                             1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 VVPSGIHY 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                    SEQUENCE FROM N.A.
                                    NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09нгн8
09нгнв;
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9X2E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TM1822
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           оэнгна
```

ö

Gaps

ö

윱

ð

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                  Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; mophilic cyanobacterium Thermosynechococcus elongatus BP-1."; mophilic syanobacterium EMBL, AP005374; BAC09170.1; -. GMBL ABA; 113205 MW; 00B9C13F0F636D2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.1%; Score 37; DB 16; Length 1044; 63.6%; Pred. No. 98; 2; Indels 0.ive 2; Mismatches 2; Indels 0
                                                                                                                                             elongatus)
                                                                                                                           Synechococcus elongatus (Thermosynechococcus elongatus
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Multidrug efflux transporter.
```

44444

셤

ઠે

```
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. Alaska;
MEDLINE=21231727; PubMed=11333309;
Bassa N., Matsushita Y., Nakamura T., Nyunoya H.;
"The Molecular Characterization and in situ Expression Pattern of Pea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-96020672; PubMed=7476204;
Moses B.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECURNCE FROM N.A.
MEDLINE-9625263; PubMed=8654969;
Billington 8.J.; Sinistraj M., Cheetham B.F., Ayres A., Moses E.K.,
KALZ M.B., Rood J.I.;
"Identification of a native Dichelobacter nodosus plasmid and
implications for the evolution of the vap regions.";
EMBL; U02462; AAB12366.1; -
InterPro; PRE00137; BRCT.
InterPro; PRE00137; BRCT.
SMART; SM00292; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteroides nodosus (Dichelobacter nodosus).
Bacteria, Proteobacteria, Gammaproteobacteria, Cardiobacteriales,
Cardiobacteriaceae, Dichelobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A multiple site-specific DNA-inversion model for the control phase and antigenic variation in Dichelobacter nodosus."; Mol. Microbiol. 17:183-196(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.3%; Score 36; DB 10; Length 91
45.5%; Pred. No. 1.2e+02;
ive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AB048713; BAB39155.1; -
InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR005202; GRAS.
InterPro; IRR005202; GRAS.
InterPro; IRR005202; GRAS.
InterPro; IRR005202; GRAS.
InterPro; IRR005202; GRAS.
INTERPROSITE; PS00588; FLAGELIA BB ROD; 1.
SEQUENCE 819 AA; 90372 MW; 41B67BD6DC72ADFA CRC64;
                                                                                                                                                                                                            (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                    819 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last seqn 01-DEC-2001 (TrEMBLrel. 19. Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                       PRT,
                                                                                                                                                                                                                                                                                                                                                             Pisum sativum (Garden pea).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Query Match
Best Local Similarity 45.5%;
Best Local Similarity 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 DDVVPTSLHFS 353
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 BEVVPXGMHYS 11
      235 EMIVPAGLHP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA ligase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=870
                                                                                                                                                                                                            01-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                     SCARECROW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q57489
Q57489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rood J.I
                                                                                                                                                       09AVK4
                                                                                                                                                                                                                                                                                                                              PSSCR.
                                                                                      RESULT 8
099AWK
1D 099AW
AC 099AW
AC 099AW
DT 01-JT
DT 01-JT
DT 01-JT
DT 01-JT
DT 01-M
DE SCAR
CO SPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=C.striatum, STRAIN=M82B,
MEDLINE=20194806; PubMed=10732668;
Tauch A., Krieft S., Kalinowski J., Puhler A.,
Tauch A., The Striatum of Process of the striatum of the striatum clinical solate Corynebacterium striatum M82B is composed of DNA segments initially identified in soil bacteria and in plant, animal, and human
                                                                                                                                                                                                                                                       SPECIES=C.xerosis; STRAIN=W82B;
MEDLINE=96117603; PubMed=8559800;
Tauch A., Kassing F., Kalinowski J., Puhler A.;
The Corynabacterium xerosis composite transposon Tn5432 consists of
two identical insertion sequences, designated IS1249, flanking the
erythromycin resistance gene ermCX.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21555285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                         Corynebacterium striatum.
Bacteria, Actinobacteridae, Actinomycetales,
Corynebacterinaes, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1725, 43770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.3%; Score 36; DB 16; Length 252; 50.0%; Pred. No. 34; 2: Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 50.0%; Pred. No. 27; 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Gen. Genet. 263:1-11(2000).

EMBL; U21300; AAC95478.1; -.

EMBL; AF024666; AAG91390.1; -.

Hypothetical protein; Plasmid.

SEQUENCE 208 AA; 23012 MW; PIS04BEIECDE85A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 8:205-213(2001).
EMBL, AP003586; BAB779299.1; -
Hypothetical protein; Complete protecme.
SEQUENCE 252 AA; 28831 WW; 925572DASD1CA519 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2002 (TrEMBLrel. 20, Created)
1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Alr1563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 AA
Hypothetical 23.0 kDa protein (GcrA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anabaena sp. (strain PCC 7120)
                                                             Corynebacterium xerosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 DVIPECKHYA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Cyanobac
NCBL_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogens."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBYWP1;
```

Q8YWP1

ò

RESULT 7 Q8YWP:

Best Loc Matches

ઠે a

ö

Gaps

ö

Length 819;

of Omp1

233 AA

PRT;

```
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4096;
                                                                                                           01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                  KREBP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSLWSO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9LW50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
Q9LW50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SO DE RETT TANKER OCCOCOS DE LA PRINCIPA DEL PRINCIPA DEL PRINCIPA DE LA PRINCIPA DEL PRINCIPA DEL PRINCIPA DE LA PRINCIPA DE 
                                        SO DE RESTRESE DE LA PROPERTICIO DEL PROPERTICIO DE LA PROPERTICIO DE LA PROPERTICIO DE LA PROPERTICIO DEL PROPERTICIO DEL PROPERTICIO DEL PROPERTICIO DE LA PROPERTICIO DEL P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECONTINE-20365717; PubMed=10910347;

SIMDBOON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi B.D., Bordin S., Bove J.M., Briones M.R.S., Barros M.H., Bonaccorsi B.D., Bordin S., Bove J.M., Briones M.R.S., Rabenco M.R.P., Camargo L.E.A., Carraro D.M., Carrer H., Rabenco M.R.P., Colombo C., Costa M.C.R., Costa-Neto C.M., Columbo L.L., Cristofani M., Dias-Neto E. Docena C., Bl-Dorry H., Racion M. B., Ferincani A.P., Rarico M.C., Franco M.C., Franco M.C., Franco J.S., Franca S.C., Franco M.C., Frohme M., Fully J. A., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P., Roper T.B., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C., Rrieger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C., Ray Lemos E.G.M., Madeira H.M.F., Marino C.L., Rarduado M.A., Madeira A.M.B., Madeira H.M.F., Marino C.L., Marcues M.V., Marcia A.M.B., Madeira H.M.F., Marino C.L., Marcues M.V., Marcia B.C., Miyaki C.T., Motto L.E.S., Manni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Adelia M.A., Adelia M.M. A., Adelia M.M. Marcue M.C., de Oliveira M.C., de Suza A.J.M., Rade Solva A.B., Santelli R.V., Sawaaski H.B., Ade Souza A.P., Terenzi M.P., Terenzi
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylella fastidiosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%; Score 35; DB 16; Length 156; 55.6%; Pred. No. 32;
                                                                                                                                                                         Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406:151-159(2000).

EMBL, AB004014; AAP04752.1; -
Hypothetical protein; Complete proteome.

SEQUENCE 156 AA; 17144 MW; D8358619C6671A5D CRC64;
                                                                         1
139 AA; 15052 MW; BOB110AA4B7D4709 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein Xf1950.
                                                                                                                                                                             62.5%; Score 35; DB 2; 55.6%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                   3; Mismatches
   PS50172; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||::| |:|
EEILPQGVH 127
                                                                                                                                                                                                                                                                                                                         3 VVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                              :|| |:|
21 IVPAGVHWS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGMH 9
                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=9a5c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
                                                                             NON TER
SEQUENCE
PROSITE;
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PC35
Q9PC35;
                                 Ligase.
                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9PC35
   8 7 7 8
8 7 7 8
                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

RESULT 11

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20399450; PubMed=10945353;
Kitchinas, Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
Kitchina S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
Characterization of gene expression of NSRRPs, transcription factors
of basic PR genes from Nicotiana sylvestris.";
Plant Cell Physiol. 41:817-824 (2000).
EMBL; AB016264; BAA97122.1;
HSSP; 080337; 2GCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, lamiids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana sylvestris (Wood tobacco).

Makaryota, Viridiplantae; Streptophyta; Maryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                   SECUENCE FROM N.A.

STRAINB-BY4; TISSUB-Leaf;
MEDLINE-95276459; PubMed-7756828;
Ohme-Takagi M., Shinshi H.;
"Ethylene-inducible DNA binding proteins that interact with an ethylene responsive element.";
Plant Cell 7:173-182(1995).
EMBL; D38126; BAA77324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%; Score 35; DB 10; Length 233; 60.0%; Pred. No. 50; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%; Score 35; DB 10; Length 237; 60.0%; Pred. No. 51; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23V AA; 26243 MW; 01BC3EBB51B46298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25563 MW; 6CD16783582C0CB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
8thylene-responsive element binding factor.
                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 AA.
     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                    Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 1.
ProDom; PD001423; TF ERF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSPAC; T02654; ...
InterPro; IPR01471; TP ERF.
Pfam; PF00847; AP2-domaIn; 1.
Brobom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
                          01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23,
(TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match

Query Match

Best Local Similarity 60.00,

Best Local 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BBVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00380; AP2; 1
SEQUENCE 237 AA: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 QAVVPKGRHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۵
```

94 QAVVPKGRHY 103

음

```
MEDLINE=93231538; PubMed=8472961; Fremaux C., De Antoni G., Raya R., Klaenhammer T.; Genetic organization and sequence of the region encoding integrative functions from Lactobacillus gasseri temperate bacteriophage phi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Engel G., Altermann E., Klein J., Henrich B.;
"Structure of a genome region of the Lactobacillus gasseri temperate phage phi adh covering a repressor gene and cognate promoters.";
Gene 210:67-70(1998).
EMBL; AJ11519; CAB55540.1; -.
InterPro; IPR002033; Glyco_hydro_25.
InterPro; IPR003646; SH3 bac.
Pfam; PF01183; Glyco_hydro_25; 1.
Probom; PD004620; Glyco_hydro_25; 1.
Probom; PD004620; Glyco_hydro_25; 1.
SMART; SM00641; Glyco_hydro_25; 1.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99384014; PubMed=10452953;
Altermann E., Klain J., Henrich B.;
"Primary structure and features of the genome of the Lactobacillus gasseri temperate bacteriophage phi-adh.";
                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=95138034; PubMed=7836307;
Henrich B., Binishofer B., Bleesi U.;
Henrich B., Binishofer B., Bleesi U.;
Lactobacillus gasseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.5%; Score 35; DB 9; Length 317; 66.7%; Pred. No. 69; 7ative 1; Mismatches 2; Indels
                                                                                                                                                                                                        Altermann B.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34703 MW; 9FF2715EE43561C7 CRC64;
                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                            317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                               Lactobacillus bacteriophage phi adh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                              PRT;
                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23, R10D12.10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          Gene 236:333-346(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 126:61-66(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 VVPMGYHYA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XVK4,
Q9XVK4,
01-NOV-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                             038317;
                              038317
                                                                                                  Lysin.
RESULT 13
Q38317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                             BHHHAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
Arabidopais thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
R10D12.10.
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-EV. COlumbia; Viscolumbia; Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S. Li J., Krementskaia I., Luros J., Ngan I., Gonzalez A., Altafi Araujo R., Chao Q., Com L., Conway A.B., Dunn P., Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M., Hazar L., Kim C., Rowley D., Shinn P., Walker M., Abayis R.W., Ecker J.R., Federspiel N.A., Theologis A.; Arabidopsis thaliana chromosome 1 BAC TSIS sequence."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; Score 35; DB 10; Length 510; 60.0%; Pred. No. 1.2e+02; 1ve 2; Mismatches 2; Indels
                                                                                                                                                                                                               'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 35; DB 5; Length 425;
50.0%; Pred. No. 95;
iive 3; Mismatches 2; Indels
                                                                                                                  Percy C.M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Transferase.
SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 AA; 55089 MW; 0DC63CC41F4712F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 AA
                                                                                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
Science 282:2012-2018(1998).
SCHENCE 281109; CAB03241.1; -.
WormPep; R10D12.10; CR12690.
InterPro; IPR000719; Prot_Kinase.
Pfam; PP00069; pkinase; 1.
Probom; PD000001; Prot_Kinase; 1.
PROSITS; PSS0011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                               MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAK-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007114; MFS.
PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 BOIVPGGLQY 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 REVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 BEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| | |:|:
BEVKPPGIHF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                 SEQUENCE PROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSI8.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9SA71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
Q9SA71
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

ö

ö

Gaps

ö

Search completed: December 22, 2003, 17:51:29

Job time : 25.2667 secs

```
sequence 4, Appli
Sequence 11, Appli
Sequence 9, Appli
Sequence 82, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 8, Appli
Sequence 26805, A
Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           December 22, 2003, 16:37:03; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11,
Sequence 7, A
Sequence 7, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                           328717
                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*

1: /cgn2 6/prodate/1/laa/5A COMB.pep:*

2: /cgn2 6/prodate/1/laa/5B COMB.pep:*

3: /cgn2 6/prodate/1/laa/6A COMB.pep:*

4: /cgn2 6/prodate/1/laa/6B COMB.pep:*

5: /cgn2 6/prodate/1/laa/6B COMB.pep:*

6: /cgn2 6/prodate/1/laa/BCCMB.pep:*

6: /cgn2 6/prodate/1/laa/BCCMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-051-341-7
US-09-394-272-8
US-09-394-272-4
US-09-394-272-1
US-09-394-272-1
US-09-394-272-1
US-08-569-147-76
US-08-569-147-8
US-08-963-811-14
US-08-963-811-14
US-08-963-811-14
US-08-963-811-14
US-08-963-811-14
US-08-963-811-8
US-08-963-811-8
US-09-252-991A-26805
US-09-383-630-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-697-367-24
US-09-394-272-10
US-08-429-054A-11
US-08-718-777-7
                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-667-711B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-667-373-4
                                                                                                                                                                                                                             328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                 US-09-909-164-12
54
                                                                                                                                                        1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1049
1068
1068
1068
1068
1081
1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
1065
                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                    Scoring table:
                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
```

| | Sequence 7, Appli | Sequence 21. Appl | Sequence 21, Appl | Sequence 21, Appl | Sequence 21. Appl | Sequence 20, Appl | Sequence 22, Appl | Sequence 22, Appl | 22 | Sequence 22, Appl | 21. | Sequence 4172. Ap | 9 | Sequence 6. Appli | 4 | 4 | Sequence 6. Appli | 23, | |
|-----|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|---------------------|-----------------|-------------------|------------------|------------------|-------------------|------------------|--|
| | US-08-193-977-7 | US-08-464-517-21 | US-08-246-361A-21 | US-08-463-772-21 | PCT-US93-05000-21 | US-08-926-842B-20 | US-08-464-517-22 | US-08-246-361A-22 | US-08-463-772-22 | PCT-US93-05000-22 | US-08-926-842B-21 | US-09-107-532A-4172 | US-08-464-517-6 | US-08-463-772-6 | US-08-246-361A-4 | PCT-US93-05000-4 | PCT-US93-05000-6 | US-08-464-517-23 | |
| | н | ~ | ~ | m | 'n | m | ~ | N | ~ | Ŋ | m | 4 | ~ | ٣ | ~ | ഗ | ហ | 0 | |
| | 173 | 189 | 189 | 189 | 189 | 231 | 236 | 236 | 236 | 236 | 240 | 241 | 280 | 280 | 289 | 289 | 291 | 292 | |
| | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | |
| · · | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | . 32 | |
| | 28 | 67 | 30 | 31 | 32 | ee. | . 34 | 38 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | |
| | | | • | | | | | | | | | • | | | | | | | |

ALIGNMENTS

```
Sequence 5, Application US/08853948B

Patent No. 6210943

GENERAL INFORMATION:
TITLE OF INVENTION: THE SAME
CURRENT APPLICATION WHORE: US/08/853,948B

CURRENT FILING DATE: 1997-05-09

CURRENT FILING DATE: 1997-05-09

MUBGER OF SEQ ID NOS: 10

SEQ ID NO 5

LENGTH: 348

TIPE: PRT

TIPE: PRT

CURLENT: ABB

CURRENT FILING DATE: 1097-05-09

SOFTWANE: Patentin Ver. 2.1

SEQ ID NO 5

TIPE: PRT

CURRENT SAME
TIPE: PRT

SEQ ID NO 5

USGANUISM: Citrus unshiu
                           Patent. No. 6210943

GENERAL INPORMATION:
ACTIONAL INPORTATION:
ACTIONAL ANTHANA, TOYOTA

TITLE OF INVENTION:
TITLE OF INVENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, Asn, Asp, OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 3; Length 341;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 VIPPGMDFS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
JS-08-853-948B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-853-948B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        è
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4

US-09-394-272-10

i Sequence 10, Application US/09394272

i Betent No. 6472588

i GENERAL INFORMATION:

i APPLICANT: Haigler, Candace H.

APPLICANT: Holaday, A. Scott

i TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

ITLE REFERENCE: 201304/1000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 4; Length 1049;
Pred. No. 67;
2; Mismatches 1; Indels
               66.7%; Score 36; DB 3; Length 348; 66.7%; Pred. No. 19; 1; Indels tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                          GENERAL NO. 923013)
GENERAL NO. 923013)
GENERAL TRYORMATION:
APPLICANT: Orozco Jr., Emil M.
APPLICANT: Caimi, Perry G.
APPLICANT: Weng, Zude
APPLICANT: Tarczynski, Mitchell
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
FILE REFRENCE: BB1166 US NA
CURRENT FILING DATE: 2000-10-26
FRIOR FILING DATE: 1998-MAY-07
FRIOR FILING DATE: 1998-MAY-06
FRIOR FILING DATE: 1999-MAY-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 36; DB 66.7%; Pred. No. 20; vative 2; Mismatches
                                                                                                                                                                                              Sequence 24, Application US/09697367
Patent No. 6323015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 66.7-
Query Match
Best Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 VIPPGMDFS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436 VIPPGMDFS 444
                                                                                                              234 VIPPGMDFS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMDYS 11
                                                                                 3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Zea mays
US-09-697-367-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 10
LENGTH: 1049
                                                                                                                                                                                -09-697-367-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-394-272-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                 ઠે
```

```
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: JEAN; VOELKER, TONI; GERVAIS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 36; DB 2; Length 1068; 66.7%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MODIFICATION OF SUCROSE
                                                                                                                                                                                                                                                                                                                                                                                                                           WEDIUM TYPE: FLOPPY DISK
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,054A
FILING DATE: 26-APR-1995
CLASSIPICATION BATA:
APPLICATION NUMBER: US/08/429,054A
FILING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 10-July-1991
CLASSIPICATION DATA:
APPLICATION NUMBER: French 90402094.9
FILING DATE: 20-July-1990
CLASSIPICATION NUMBER: French 90402094.9
FILING DATE: 20-July-1990
ATTORNEY/AGENT INFORMATION:
NAME: Charles A. MMSETLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1137
TELEDHAND: (712) 6.51.9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08718777; Patent No. 5981852; GENERAL INFORMATION:
APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Woelker, T.
APPLICANT: Woelker, T.
APPLICANT: GENVAIS, M.
TITLE OF INVENTION: MODIFICATION O
Sequence 11, Application US/08429054A; Patent No. 5917126; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 11.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66.7
Matcheв 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10016
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| |||:|
435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                        CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-429-054A-11
                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-718-777-7
```

```
Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                             LENGTH: 1068 amino acids
                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-051-341-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:| |||:|
435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Zea mays US-09-394-272-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-394-272-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09051341

Patent No. 6124528

GENERAL INFORMATION:
APPLICANT: Shewmaker, C. K.
APPLICANT: Shewmaker, C. K.
TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STREET: California
COUNTRY: USA
IP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BP PC Compatible
COMPUTER: DELOGYMETER PC-DOS/MST-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 1068;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                        STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSIPICATION: 800
PRIOR APPLICATION NUMBER: US/08/718
FILING DATE: US/08/718
APPLICATION NUMBER: US/08/717
FILING DATE: 27-DEC-1993
ATYORNEY/AGRNT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
                                                                                          E: Law Offices of Barbara Rae-Venter
260 Sheridan Avenue, Suite 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGNE.072.02US
  PHOSPHATE
SYNTHASE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                             NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VVPXGMDYS 11
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-718-777-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-051-341-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
Sequence 8, Application US/09394272

| Sequence 8, Application US/09394272
| Patent No. 6472588
| GENERAL INFORMATION:
| APPLICANT: Haigler, Candace H. APPLICANT: Haigler, Candace H. APPLICANT: Holdady, A. Scott
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| CURRENT APPLICATION NUMBER: US/09/394,272
| CURRENT FILING DATE: 1999-09-10
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 8
| LENGTH: 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09394272

Sequence 4, Application US/09394272

Patent No. 6472588

GENERAL INPORMATION:

APPLICANT: Haigler, Candace H.

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS SYNTHASE

FILE REPERENCE: 201304/1000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT PILIOR DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 4; Length 1068;
Pred. No. 68;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 3; Length 1068;
Pred. No. 68;
2; Mismatches 1; Indels
FILING DATE: 25-OCT-1996

APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-OCT-1995
FRILING DATE: 27-OCT-1995
FRILING DATE: 12-AN-1995
FILING DATE: 12-AN-1995
FILING DATE: 12-AN-1995
FRILING DATE: 12-AN-1995
FRILING DATE: 12-AN-1995
FRIEGRAT INFORMATION:
NAME: BATBATA Ree-Venter. Ph.D.,
REGISTRATION NUMBER: 32,750
FREFRENCE/DOCKET NUMBER: GGNE.110.02US
TELEFAN: (415)328-4470
FREFRANCE, (415)328-4470
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
FEMALLY AND ALL STATES.
```

ò

```
A
                                                                                                                                                                                                                                                                                       STATE: PACOUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-569-147-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-394-272-9

Sequence 9, Application US/09394272

Sequence 9, Application US/09394272

Sequence 9, Application US/09394272

Sequence 9, Application US/09394272

GENERAL INFORMATION:

APPLICANT: Halgler, Candace H.

APPLICANT: Halgler, Candace H.

APPLICANT: Halgler, Candace H.

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERENCE: 201304/1000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOSTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haigler, Candace H,
APPLICANT: Haigler, Candace H,
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTHARE: PATENTIN VOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.7%; Score 36; DB 4; Length 1083; Best Local Similarity 66.7%; Pred. No. 69; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.7%; Score 36; DB 4; Length 1084; Best Local Similarity 66.7%; Pred. No. 69; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                               Score 36; DB 4; Length 1081; Pred. No. 69;
                                                                                                                                                                             1; Indels
                                                                                                                                                                             2; Mismatches
                                           ; TYPE: PRT
; ORGANISM: Craterostigma plantagineum
US-09-394-272-4
                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09394272
Patent No. 6472588
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT CRGANISM: Arabidopsis thaliana US-09-394-272-11
                                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:| |||:|
453 VIPPGMDFS 461
                                                                                                                                                                                                                                                  |:| |||:|
445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| |||:|
483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGMDYS 11
                                                                                                                                                                                                                         3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Oryza Bativa
US-09-394-272-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 11
LENGTH: 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1084
SEQ ID NO 4
LENGTH: 1081
                                                                                                                                                                                                                                                                                                                                                        US-09-394-272-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
Search completed: December 22, 2003, 16:43:43 Job time : 10.1333 secs
       LENGTH: 59
                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14

US-09-252-991A-31637

Squence 31637, Application US/09252991A

Patent No. 6521795

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31637

LENGTH: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1065;
                                                                                                                                                                                                                                                                                                                                                                                           63.0%; Score 34; DB 3; Length 140; 75.0%; Pred. No. 16; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08963851
; Sequence 14, Application US/08963851
; Patent No. 6300116
; GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
; APPLICANT: ANDERSEN, CARSTEN
APPLICANT: ANDERSEN, CARSTEN
; APPLICANT: BAUDITZ, PETER
; APPLICANT: BAUDITZ, PETER
; APPLICANT: BAUDITZ, PETER
; APPLICANT: BAUSEN, PETER KAMP
; ITLE OP INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
; CURRENT APPLICATION NUMBER: US/08/963,851
; CURRENT APPLICATION NUMBER: 1997-11-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PateSEQ for Windows Version 3.0
; SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.0%; Score 34; DB 4; I ilarity 85.7%; Pred. No. 1.7e+02; Conservative 0; Mismatches 1;
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: TRUJI110, Doreen Yarko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
FELECOMMUICATION INFORMATION:
TELECHONE: (215) 568-3100
FELEPAX: (215) 568-3439
INFORMATION FOR EQO ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
HOLECULE TYPE: protein
US-08-569-147-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 WPTGFDY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 POGMDYS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 PXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-31637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ठ
```

```
ö
                                                                                             Gaps
                                                                                             ö
                                                           Score 33; DB 4; Length 59;
Pred. No. 9.6;
4; Mismatches 2; Indels
TYPE: PRT ; ORGANISM: Enterococcus faecalis US-08-963-851-14
                                                             Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                            1::| |::||
38 EKHIPGGLEYS 48
                                                                                                                         1 BEVVPXGMDYS 11
```

```
December 22, 2003, 16:40:14; Search time 20.8667 Seconds (without alignments) 98.451 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB_pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_pep:*
13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                696363 seqs, 186758610 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                              US-09-909-164-12
54
                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| u | 946, App | 73, Appl | Sequence 168, App | Sequence 10, Appl | 3 71, Appl | e 8, Appli | 4, | 11, Appl | 7,6 | | 1660, Ap | Sequence 58, Appl | equence 5111, Ap | e 4, Appli | 4. |
|----------------------------------|-------------------|----------------------------|-------------------|-------------------|------------------|-----------------|-----------------|------------------|-----------------|------------------|--------------------|-------------------|--------------------|-----------------|-----------------|
| Description | Sequence | Sequence | Sequence | Sequence | Sequence | Seguence | Sequence | Sequence | Sequence | Sequence 27, | Sequence 1660 | Sequence | Sequence | Sequence 4, | Sequence |
| SUMMARIES | US-10-393-840-946 | US-10-289-757-73 | US-10-289-757-168 | US-10-217-700-10 | US-10-289-757-71 | US-10-217-700-8 | US-10-217-700-4 | US-10-217-700-11 | US-10-217-700-9 | US-09-813-408-27 | US-10-094-749-1660 | US-10-091-007-58 | US-09-815-242-5111 | US-10-029-120-4 | US-10-027-806-4 |
| DB | 12 | 12 | 12 | 15 | 12 | 15 | 15 | 15 | 15 | 11 | 12 | 12 | σ | 12 | 14 |
| * Query Match Length DB ID | 126 | 937 | 938 | 1049 | 1062 | 1068 | 1081 | 1083 | 1084 | 440 | 588 | 222 | 1062 | 3472 | 3472 |
| % Query Match | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 64.8 | 63.9 | 63.0 | 63.0 | 63.0 | 63.0 |
| Score | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 35 | 34.5 | 34 | 34 | 34 | 34 |
| Result No. | - | 7 | m | 4 | 5 | 9 | 7 | æ | σ | 10 | 11 | 12 | 13 | 14 | 15 |

| Sequence 4, Appli Sequence 14, Appli Sequence 14, Appli Sequence 12076, A Sequence 1267, A Sequence 1267, A Sequence 526, App Sequence 526, App | |
|---|--|
| -10 - 034 - 623 - 4 -10 - 027 - 801 - 4 -10 - 029 - 386 - 320 -10 - 029 - 386 - 526 - 488 -10 - 029 - 978 - 526 - 526 -10 - 978 - 526 - 526 -10 - 978 - 628 - 526 -10 - 978 - 628 - 526 -10 - 978 - 1978 - 1978 - 526 -10 - 978 - 1978 - 978 | US-09-978-643A-526 US-09-978-375A-526 US-09-978-188A-526 US-09-978-298A-526 |
| 440110000001111111111111111111111111111 | 1221 |
| 8.82 2.22 2.22 3.22 3.22 3.22 3.22 3.23 3 3.23 3 3.23 3 | 736 736 736 |
| | 61.1 61.1 61.1 |
| ************************************** | 3 M M M |
| , 11111222222222222222222224444444444444 | 4 4 4 2 6 4 7 |

ALIGNMENTS

```
US-10-393-840-96

US-10-393-840-96

Sequence 946, Application US/10393840

Publication No. US2003022992211

SEQUENCE STATE OF VARIATION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Cell Wall Polysaccharides ITILE OF INVENTION: Modification of Plant Cell Wall Polysaccharides FILE REFERENCE: 11000.1012-3

CURRENT APPLICATION NUMBER: US/10/393,840

PRIOR PLING DATE: 2003-03-20

PRIOR PLING DATE: 1998-10-13

PRIOR PLING DATE: 1998-10-13

PRIOR PLING DATE: 1998-10-13

PRIOR PLING DATE: 1998-10-13

PRIOR PLING DATE: 1999-10-13

PRIOR PLING DATE: 1999-10-14

PRIOR PLING DATE: 1999-10-16

PRIOR APPLICATION NUMBER: PCT NZ/99/00169

PRIOR PLING DATE: 1999-10-16

PRIOR PLING DATE: 1999-10-16

PRIOR PLING DATE: 1999-10-16

PRIOR APPLICATION NUMBER: PCT NZ/99/00169

PRIOR PLING DATE: 1999-10-16

PRIOR PLING DATE: 1999-10-16

PRIOR PLING DATE: 1999-10-16

PRIOR PLING DATE: 1999-10-16

PRIOR APPLICATION NUMBER: PCT NZ/99/00169

PRIOR PLING DATE: 1999-10-16

PRIOR PLING DATE: 1999-10-16

PRIOR PLING DATE: 1999-10-16

PRIOR PLING DATE: 1999-10-13

PRIOR PLING DATE: 1999-10-10

PRIOR PLING DATE: 1999-10-13

PRIOR PLING
```

ö

RESULT 2 US-10-289-757-73

```
Sequence 10, Application US/10217700

Publication No. US20030070191A1

GENERAL INFORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Haigler, Candace H.

APPLICANT: Holaday, A. Scott

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: WIMBER: US/10/217,700

CURRENT FILING DATE: 20134/1000

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LINGTH: 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 36; DB 15; Length 1049; 66.7%; Pred. No. 1.5e+02; ive 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 12; Length 1062;
Pred. No. 1.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 71, Application US/10289757

Publication No. US20030180751A1

GENERAL INFORMATION:

APPLICANT: Demmer, Jeroen

APPLICANT: Demmer, Jeroen

APPLICANT: Gibson, John Bryan

APPLICANT: Shenk, Michael Andrew

APPLICANT: Saulsbury, Keith Martin

APPLICANT: Glann, Matthew

APPLICANT: Hall, Claire

TITLE OF INVENTION: Grasses and methods for their use

FILE REFERRENCE: 11000.1061U

CURRENT FILING DATE: 2002-11-07

PRIOR PRICATION NUMBER: 60/337,703

PRIOR PRICATION DATE: 2001-11-07

NUMBER: OF TRIVER CONTINUED TO THE CONTINUED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 218
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      %30-217-700-8

%Sequence 8, Application US/10217700
% Publication No. US20030070191A1
% GENERAL INFORMATION:
% APPLICANT: Haigler, Candace H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPB: PRT
ORGANISM: Festuca arundinacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 VIPPGMDFS 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:| ||:|
436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Oryza sativa
US-10-217-700-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 71
LENGTH: 1062
         US-10-217-700-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-289-757-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-289-757-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.7%; Score 36; DB 12; Length 938; Best Local Similarity 66.7%; Pred. No. 1.3e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 66.7%; Score 36; DB 12; Length 937; Local Similarity 66.7%; Pred. No. 1.3e+02; nes 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dement of the control of 
                                                                                                                                                                      APPLICANT: Posser, Richard L
APPLICANT: Posser, Richard L
APPLICANT: Sherk, Wichael Andrew
APPLICANT: Sherk, Wichael Andrew
APPLICANT: Sherk, Wichael Andrew
APPLICANT: No. US20030180751Alriss, Geoffrey
APPLICANT: Allabury, Keith Martin
APPLICANT: Saulsbury, Keith Martin
APPLICANT: Balls Clair
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Grasses and methods for their use
TITLE REFERENCE: 11000.1061U
CURRENT APPLICATION NUMBER: US/10/289,757
CURRENT PILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73
LENGTH: 937
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-289-757-168
. Sequence 168, Application US/10289757
. Publication No. US20030180751A1
. GENERAL INFORMATION:
Sequence 73, Application US/10289757
Publication No. US20030180751A1
GENERAL INFORMATION:
APPLICANT: Demmer, Jeroen
APPLICANT: Porster, Richard L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Lolium perenne
US-10-289-757-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Lolium perenne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1:| |||:|
462 VIPPGMDFS 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 462 VIPPGMDFS 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-289-757-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

Matches

RESULT 3

g

ઠે

ö

Gapa

ö

Gaps

RESULT 4

셤

ઠે

```
LENGTH: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 27
                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                        유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-217-700-11

Sequence 11, Application US/10217700

Publication No. US20030070191A1

GENERAL INFORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Holaday, A. Scott

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERENCE: 201304/1000

CURRENT PILING DATE: 2002-08-12

EARLIER APPLICATION NUMBER: 09/394,272

EARLIER FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10217700
Publication No. US20030070191A1
GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT PILING DATE: 2002-081.2
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOUTHARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
APPLICANT: Holaday, A. SCOLT
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT FILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO S. 20
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.7%; Score 36; DB 15; Length 1081; Best Local Similarity 66.7%; Pred. No. 1.6e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 36; DB 15; Length 1068; 66.7%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Craterostigma plantagineum
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| |||:|
435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| |||:|
445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Zea mays
US-10-217-700-8
                                                                                                                                                                                                                                                        1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-217-700-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-217-700-4
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
Sequence 27, Application US/09813408
Publication No. US20030049619A1
GENERAL INFORMATION
APPLICANT: Delagrave, Simon
APPLICANT: Delagrave, Simon
TITLE OF INVENTION: Methods For The Synthesis Of Polynucleotides And Combinatorial
TITLE OF INVENTION: OF Polynucleotides
FILE REPERENCE: HERO041
CURRENT APPLICATION NUMBER: US/09/813,408
CURRENT PILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                              US-10-217-700-9

Sequence 9, Application US/10217700

Sequence 9, Application US/10217700

Publication No. US20030070191A1

GENERAL INFORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Holaday, A. Scott

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERENCE: 201304/1000

CURRENT FILING DATE: 2000-08-10

EARLIER APPLICATION NUMBER: 09/394,272

RARLIER FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9
                                                                                                                                                                         Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                         Length 1083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 36; DB 15; Length 1084; 66.7%; Pred. No. 1.6e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.8%; Score 35; DB 11; Length 440; 66.7%; Pred. No. 92; tive 2; Mismatches 1; Indels
                                                                                                                 Query Match
66.7%; Score 36; DB 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1;
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-217-700-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Aeropyrum pernix
US-09-813-408-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                         483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||:| |:||
120 EVLPWGVDY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 VIPPGMDFS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
US-10-217-700-9
                                                                                                                                                                                                                3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-813-408-27
```

```
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/029,120
CURRENT FILING DATE: 2001-12-1
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.0%; Score 34; DB 9; Length 1062; 85.7%; Pred. No. 3.9e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DAISELDECK, KOLDELL
APPLICANT: Oblien, Kari L.
APPLICANT: Zyekind, Judith W.
APPLICANT: Zyekind, Judith W.
APPLICANT: Zyekind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
FILE OF INVENTION: Prokaryotes
FILE REFERENT ELITRA.011A
TITLE OF INVENTION: Prokaryotes
FILE REPERENT SELITRA.011A
CURRENT APPLICATION NUMBER: 06/191,078
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR PLING DATE: 2000-05-21
FRIOR PLING DATE: 2000-05-23
FRIOR PLING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 60/223,625
FRIOR PLING DATE: 2000-10-23
FRIOR PLING DATE: 2000-11-27
FRIOR PRING DATE: 2000-11-27
FRIOR PLING DATE: 2000-11-27
FRIOR PLING DATE: 2000-11-27
FRIOR PLING DATE: 2000-11-27
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2
  2; Indels
  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                             US-09-815-242-5111
; Sequence 5111, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10029120 Publication No. US20030175708A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7°
  5; Conservative
                                                                                         :::|| | ||
201 KKIVPIGFDY 210
                                                     1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 POGMDYS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 PXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Pseu
US-09-815-242-5111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-029-120-4
  Matches
                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.5; DB 12; Length 588;
Pred. No. 1.6e+02;
1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 12; Length 222;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wells, Jeremy M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Microbial Technics limited
APPLICANT: Le Page, Richard W F
APPLICANT: Le Page, Richard W F
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REPERENCE: PWC/P21978WO
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: GB 9921125.2
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 276
SOFTWARE: Patentin version 3.0
SENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REPERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
                                                                                Sequence 1660, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-091-007-58
; Sequence 58, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
                                                                                                                                                              APPLICANT: 150GAI, TAKAO
APPLICANT: 150GAI, TOMOYASU
APPLICANT: 0TSUKI, TETSUJI
APPLICANT: 0TSUKI, TETSUJI
APPLICANT: 15HII, SHIZUKO
APPLICANT: 15HII, SHIZUKO
APPLICANT: 15HII, SHIZUKO
APPLICANT: 15ONO, YUUKO
APPLICANT: 15ONO, YUUKO
APPLICANT: 15ONO, YUKO
APPLICANT: 15ONO, YUKO
APPLICANT: 15ONO, YUKO
APPLICANT: 0TSUKA, KAORU
APPLICANT: 0TSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1660
LENCTH: 588
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAGAHARI, KENJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 EEVVP-GMDF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-094-749-1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
```

```
Sequence 4, Application US/10027806;
Publication No. US2002016047641
; GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP. 1057, 806
CURRENT APPLICATION NUMBER: US/10/027, 806
CURRENT PILING DATE: 2001-12-21
FRIOR PILING DATE: EARLIER PILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                         ö
                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 14; Length 3472;
Pred. No. 1.5e+03;
4; Mismatches 2; Indels 0; Gaps
                                                                                                                                                         ö
                                                                                                         Query Match 63.0%; Score 34; DB 12; Length 3472; Best Local Similarity 45.5%; Pred. No. 1.5e+03; Matches 5; Conservative 4; Mismatches 2; Indels (
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-029-120-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                          2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMDYS 11
                                                                                                                                                                                               1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                       RESULT 15
US-10-027-806-4
                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                        요
```

Search completed: December 22, 2003, 17:32:43 Job time : 20.9333 BecB

|:|:| |: | 2294 EDVIPRGISFS 2304

8 3

virus
virus
virus
virus
virus
virus
virus
virus
virus

virus virus virus virus virus virus

Hepatitis Hepatitis

virus virus

virus virus virus

virum virum virue

٠,

OM protein

Run on:

Sequence:

searched:

Database

40000

Result No.

₹ & E

```
/note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "D-form residue"
          ABB80525
ABB80526
ABB80526
ABB80526
ABB80551
ABB80551
ABB80557
ABB80559
ABB80566
ABB80566
ABB80566
ABB80567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80524 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001; 2001WO-US23169
  (first entry)
  11
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80524
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80524
 Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                        2003, 16:41:00 ; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec
                                                                                                                                                                                                                                                                                                             A Geneseq 197un03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq-geneseq-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq-geneseq-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq-geneseq-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseq-geneseq-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-geneseq-genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                  1107863
          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                             1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80528
ABB80529
ABB80561
ABB80562
ABB80538
ABB80542
ABB80543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80524
                                                                                                                                                                        0.5
                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ωï
                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                  US-09-909-164-12
54
                                                                                                                                        EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333333333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                          December 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                    - protein search,
                     Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.3
96.3
96.3
96.3
96.3
87.0
87.0
                                                                                                                               score:
                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
52
52
52
52
54
74
47
46
46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
```

Gaps

;

Length 11; Indels

Novel

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                               96.3%; Score 52; DB 23;
100.0%; Pred. No. 0.0018;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80529 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 64; 69pp; English.
                                                                    Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                  Local Similarity 100.
hes 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                       1 BEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-361643/39
                                                                                                                                                                                                                                                  11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200208251-A2
                                    virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB80529;
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                          peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 52; DB 23; Length 11; 100.0%; Pred. No. 0.0018; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Norvalyl care residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunck TK;
                                                                        Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80528 standard; peptide; 11 AA.
                                                                                                                                                                                                                Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2001; 2001WO-US23169
 21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                                    (CORV-) CORVAS INT INC
                                                                         Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-361643/39
                                                                                                       WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200208251-A2
                                                                                                                                                                               virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                      Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /irucide.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80528;
```

Query Match

Matches

ABB80528

셤

ò

```
is useful for treating disorders associated with hepatitis C virus
                                                                                                                                      RESULT
   ខ្លង្គបូ
                                                                                    ઠે
                                                                                                     셤
                                                                                                                                                                    ö
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-keroamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41
                                                                                                                             ö
                                                                                                         Length 11;
                                                                                                      Score 52; DB 23; Length 11; Pred. No. 0.0018; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note≈ "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunck TK;
                                                                                              96.3%; Scc.
100.0%; Pre
                                                                                                                                                                                                                      ABB80561 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                            Conservative
                                                                                                                                                1 EEVVPXGMDYS 11
                                                                                                                                                                   EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-361643/39
                                                                                                                Local Similarity
les 11; Conserv
                                                                                    11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus protease
                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lim-wilby M,
                                                                                                                                                                                                                                                                08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                            ABB80561;
                                                                                                                                                                                                                                                                                                                     virucide.
                                                                                    Sequence
                                                                                                      Query Match
                                                                                                                          Matches
                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                             ABB80561
   888888888888
                                                                                                                                                                  셤
                                                                                                                                                ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
                                                                                  ö
                                         Length 11;
                                                                                Indels
                     DB 23; Le...
                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "C-terminal amide"
                                       Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                       96.3%; Sco.
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                     ABB80562 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                Conservative
                                                                                                                         ።
                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note∍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lim-wilby M, Levy OE,
                                                                                                                       EEVVPXGMDYS
                                                                                                                                                            EEVVPXCMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-361643/39.
                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AA;
11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-Bite
                                                                                                                                                                                                                                                                                                                                                       08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
Sequence
                                                                                                                                                                                                                                                                                                                ABB80562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
```

ABB80538 RESULT

g ò

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                             "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 23; Length 11; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                            note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                               'note= "D-form residue"
                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80543 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŢĶ;
                                                  ABB80542 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 87.0%;
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEVVPXGQDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200208251-A2
                                                                                                                                                                                                                                                                              Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                     08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2002
                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80543;
                                                                                                                                                                                                         virucide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80543
                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                    ö
Score 52; DB 23; Length 11;
Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.0%; Score 47; DB 23; Length 11; 90.9%; Pred. No. 0.017; ive 0; Mismatches 1; Indels
                                  0; Indels
          100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                       ABB80538 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunck
 96.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEVVPXGQDYS 11
                                                                  1 EEVVPXGMDYS 11
                                                                                                    EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-361643/39.
                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                            08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                          ABB80538;
                                                                                                                                                                                                                                                                                                                                               virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                    Matches
```

ö

Gaps

ö

1; Indels

(first entry)

08-OCT-2002

ò 셤

```
"Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                    compound having hepatitis C virus protease inhibitory al for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 23; Length 11;
Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "N-terminal acetyl"
                                                                'note= "N-terminal acetyl"
                                                                                                                                                "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
/note= "D-form residue"
                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     ŢĶ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80522 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                     Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.2%;
90.9%;
                                                                                                                                                                                                                                                                                   21-JUL-2000, 2000US-220101P
                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                               11
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMDYS 11
                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                  Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 REVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Novel peptide co
activity useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus protease
                                                                                                                                                                                WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                               Modified-site
                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-2002
                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virucide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
8X5CCCCCCCX8X4444X6X5X5X5X5X6X6X4444444444888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide compound having hepatitis C virus protease inhibitory ty useful for treating disorders associated with hepatitis C
               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 23; Length 11;
Pred. No. 0.017;
0; Mismatches 1; Indels
                                                                                                                                                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                 'note= "D-form residue"
                                                                                                                                                                                                                                                note= "D-form residue"
                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą.
                                                                                                                                                                                               /note= "Norvalyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB80521 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levy OB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BEVVPXGQDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 REVVPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AA;
                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease
                                                                                                                                                                                                                                                                                                                                                #0200208251-A2
                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                               Modified-site
                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                               Synthetic.
                                                             virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
```

Novel virus

RESULT 9

0×2×6×8×2××

Š 셤

ö

Gaps

```
/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 23;
Pred. No. 0.026;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŢĶ;
                                                                              ŢĶ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ż
                                                                                                                                                                                                          Claim 17; Page 64; 69pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunck
                                                                              Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80526 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                     85.2%;
90.9%;
                21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 90.5
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
                                              (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 REVVPXGMDYS
                                                                                                              WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
                                                                                                                                                                                                                                                                                                                                                                       11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                            virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lim-wilby M,
                                                                              Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                   hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invudide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                     represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "N-terminal acetyl"
                /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                           Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80525 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.2%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169
                                                                                                                                            21-JUL-2000; 2000US-220101P
                                                                                                              19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                           Levy OE,
                                                                                                                                                                            (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEVVPXGMSYS
                                                                                                                                                                                                                                          WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AA;
                                                                                                                                                                                                                                                                                                           virus protease
                                                WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-Bite
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-Bite
                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                          Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-2002
                                                                            31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

Matches

RESULT 11

g

ઠે

Gape

; 0

ï

Length 11;

Score 46; DB 23; Pred. No. 0.026; 0; Mismatches

85.2%; 90.9%;

11 11

```
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have frucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                     ABB80548 standard; peptide; 11 AA.
                                                                                              Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                           1 EBVVPXGMDYS
                                                                                                                                                                 1 BEVVPXGTDYS
                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Σ
                                                                                                                                                                                                                                                                  08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2002
                                                                                                                                                                                                                                                                                                            Hepatitis (virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim-wilby
                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                             Sequence
                                                                                                                                                                                                                                            ABB80548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel
                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                            ABB8054
  8888888
                                                                                                                                                              셤
                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                            of the
                                                                                                                                                      ingredient
                                                                                             The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                         a medicament to treat disorders associated with HCV protesse. A pharmaceutical composition comprising the peptide as an active ing is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                            DB 23; Length 11;
                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                     . 0.026;
                                                                                                                                                                                                           Score 46; DB 2
Pred. No. 0.026
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  ABB80547 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brunck TK;
                                                                          Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Norvaly1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                           85.2%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                     Query Match
Best Local Similarity 90.9
                                                                                                                                                                                                                                                                           1
                                                                                                                                                                                                                                                      1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                    BEVVPXGMSYS
           WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-361643/39
                                                                                                                                                                                      11 AA;
                                                      virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                            08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                      ABB80547;
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                virucide
                                                                                                                                                                                                                                                                                                                      ABB80547
                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                          셤
```

```
/note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                      C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.
                                                                                                                                                                                                                                                                                                                                         'notes "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "D-form residue"
                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     īĶ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-220101P
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levy OB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
```

```
Search completed: December 22, 2003, 17:41:01 Job time : 32.4667 secs
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                           "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                              Gaps
                                                                                                                                                                                                                                                        Hepatitis C virus, HCV; serine protease, inhibitor, alpha-ketoamide, virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease -
                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
                              ö
Score 46; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                   /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                    note= "D-form residue"
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                ABB80551 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.2%;
90.9%;
  85.2%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.9'
Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                      1 EEVVPXGMDYS 11
                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200208251-A2
                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                    08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002.
                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                          ABB80551;
                                                                                                                     RESULT 15
                                                                                                                                   ABB80551
                                                                               g
                                                                                                                                                              ઠે
```

Gapa

ö

1 EEVVPXGMDYS 11 FEVVPXGSDYS 11

g

ઠે

ч

```
; Search time 9.06667 Seconds (without alignments) 116.675 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                     283308
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                           283308 seqs, 96168682 residues
                                                                                                               December 22, 2003, 17:24:36
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                       US-09-909-164-12
54
1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                             Run on:
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | hypothetical prote | ρ | V1 protein - tobac | sucrose-phosphate | sucrose-phosphate | unknown protein F2 | sucrose-phosphate | sucrose-phosphate | sucrose-phosphate | sucrose-phosphate | sucrose-phosphate | hypothetical prote | peptidoglycan-bind | probable alkaline | hypothetical prote | probable membrane | fat facets (faf) s | plastocyanin b - L | plastocyanin precu | plastocyanin b pre | 6-O-methylguanine- | O6-methylguanine-D | hypothetical prote | probable hexosyltr | L-lactate dehydrog | ABC transporter AT | phenylalanine-tRNA | succinate dehydrog | disease resistance |
|-----------|-----------------------|--------------------|--------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | 8 | S54619 | D69551 | A42452 | S72649 | 872650 | G96764 | JC4783 | JQ1329 | T09837 | T04062 | T04103 | T24111 | H87660 | H72784 | T20173 | F69009 | B49132 | 800210 | 838255 | S58208 | AG3104 | D98182 | P72745 | G69290 | G69350 | E86665 | A70164 | F81138 | T48898 |
| | 80 | 2 | N | ~ | N | ĸ | N | ~ | - | N | N | N | ~ | ~ | ĸ | N | N | N | ~ | N | N | ~ | 7 | 7 | - | 7 | 7 | 7 | ~ | 0 |
| | Query Match Length | 156 | 363 | 102 | 341 | 348 | 460 | 1049 | 1068 | 1081 | 1083 | 1084 | 425 | 433 | 440 | 1150 | 1474 | 2747 | 66 | 155 | 168 | 290 | 290 | 296 | 357 | 366 | 265 | 999 | 587 | 906 |
| d | Ouery Match | 74.1 | 70.4 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 64.8 | 64.8 | 64.8 | 64.8 | | 64.8 | | 63.0 | | 63.0 | | 63.0 | • | | • | • | 63.0 | 63.0 |
| | Score | 4 | 38 | 36 | 36 | 36 | .36 | 36 | 36 | 36 | 36 | 36 | 35 | 35 | 35 | 35 | 35 | 35 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 |
| | Result No. | | 7 | m | 4 | S | φ | 7 | & | σ | 10 | 11 | 12 | 13 | | 15 | 16 | 17 | 18 | 19 | 50 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 |

| disease resistance RND multidrug effl | hypothetical prote hypothetical 367K | partial transposas hypothetical prote | fibroblast growth | hypothetical proce | unknown protein [i transposase ISC105 | transposase ISC105 hypothetical profe | pantoate-beta-alan transposase ISC105 |
|--|---|--|-------------------|--------------------|--|--|--|
| T48899 F83335 | T30830 T31308 | A99427 A90471 | S27021 R90335 | S57810 | A96546 F90298 | C90307 C64417 | G83055 E90487 |
| 0 0 | 04 | 0 0 | 0,0 | 100 | 100 | ~ ~ | 0 0 |
| 908 | 1062 3472 | 97 128 | 172 | 225 | 257 | 267 | 283 |
| 63.0 | 63.0 63.0 | 61.1 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 61.1 |
| 9.9 4.4 | а в 4 4 | 9 93 9 93 | 60 60 60 60 | 0 0 0 | . e. e. | e e | 333 |
| 30 31 | 33.2 | 3 4 3 5 | 36 | | 4 4 4 1 | 4 4 2 6 | 4 4 4 0 |

ALIGNMENTS

| RESULT 1 S54619 humothatical arotain VOB0134 - yeart (Canabaramoon commission) | |
|--|------------|
| " | |
| C.Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002 C.Accession: 854619; 866879 | |
| Ride Haan, M.; Maarse, A.C.; Grivell, L.A. submitted to the RMBL Data Library. May 1995 | |
| A, Reference number: S54617 | |
| A; Molecule type: DNA | |
| AfResidates: 1-156 collection with any and the second and the seco | |
| A.t.Cost-teresciences ambulato.sii Naligitutossi ribni-CAMOUTOS.ii rib:g823123 Ride Haan, M.: Grivell, L.A.: Maarse, A.C | |
| submitted to the Protein Sequence Database, July 1996 | |
| A;Reference number: S66877 | |
| A, Accession: S66879 | |
| A; Molecule type: DNA | |
| Ajkebalduesi 1.156 kolbw. Ajkrosa-references RMRH.274920. NID.41420100. DION.62800201 1. DID.4142011. MIDG.VOL | 100. ag 14 |
| A; Experimental source: strain 5288C | 101:53:10 |
| C;Genetics: | |
| A;Cross-references: SGD:S0005539 | |
| A;Map position: 15R | |
| C, Superfamily: hypothetical protein YOR013w | |
| Query Match 74.1%; Score 40; DB 2; Length 156; | |
| _ | |
| QY 2 EVVPXGMDY 10 | |

50 EVMPLGMDY 58

셤

conserved hypothetical protein AF2411 - Archaeoglobus fulgidus

Ciprerion introduction of the control of the contro

```
unknown protein F25P22.17 [imported] - Arabidopsis thaliana
unknown protein F25P22.17 [imported] - Arabidopsis thaliana
GiSpecies: Arabidopsis thaliana (mouse-ear cress)
GiAccession: 40-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
GiAccession: 40-Mar-2001
GiAccession: 40-Mar-2001
GiAccession: 40-Mar-2001
GiAccession: 50-Mar-2001
GiAccession: 50-Mar-2001
GiAccession: 50-Mar-2001
GiAccession: 60-Mar-2001
GiAccession: 60-Mar-
    Bucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
C;Species: Citrus unshiu
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: 872650
R;Komateu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate synt A;Reference number: 872648; MUID:96439842; PMID:8842155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hoxosyltransferase; sucrose biosynthesis
F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
A;Relatus: nucleic acid sequence not shown
A;Rolecule type: mRNA
A;Residues: 1-348 «KOM>
A;Cross-references: ENBL:AB006660; NID:g2351059; PIDN:BAA22071.1; PID:g2351060
A;Rxperimental source: fruit, cv. Miyagawa-Wase
A;Rxperimental source: fruit, cv. Miyagawa-Wase
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: G96764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-460 <STO>
A;Cross-references: GB:AE005173; NID:g6692750; PIDN:AAF24856.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 2; Length 348;
Pred. No. 17;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 36; DB 2; Length 460;
70.0%; Pred. No. 23;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sucrose-phosphate synthase (EC 2.4.1.14)
C;Species: Oryza sativa (rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7-
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 EEDVPSAMDY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| |||:|
234 VIPPGMDFS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 WPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: F25P22.17
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: SPS3
C;Punction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Citrus unshin

C.Species: Citrus unshin

C.Accession: S72649

R.Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.

Mol. Gen. Genet. 252, 346-351, 1996

A.Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate syntha

A.Reference number: S72649; MUID:96439842; PMID:8842155

A.Accession: S72649

A.Status: nucleic acid sequence not shown

A.Katatus: nucleic acid sequence was submitted to the EMBL Data Library, August 1997

A.Experimental source: fruit, cv. Miyaqawa.Wase

A.Katatus: he nucleotide sequence was submitted to the EMBL Data Library, August 1997

A.Gene: SPS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.
A;Trile: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld
A;Reference number: A42452; MUID:92188538; PMID:1546458
A;Molecule type: DNA
A;Residues: 1-363 «KLE»
A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose A;Pathway: sucrose biosynthesis
(S,Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;1-341/Domain: sucrose-ksucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%; Score 36; DB 2; Length 341; llarity 66.7%; Pred. No. 16; Conservative 2; Mismatches 1; Indels
                                                                                                                                                Query Match 70.4%; Score 38; DB 2; Length 363; Best Local Similarity 54.5%; Pred. No. 6.8; Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 2; Length 102;
Pred. No. 4.3;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| |||:|
228 VIPPGMDFS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-102 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A42452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                    а
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

Gaps

ö

ö

Gaps

ö

RESULT 5

ಶ

ដ

```
A,Map position: 4
A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3;
A;Note: P28M11.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
P;176-674/Domain: sucrose/sucrose-phosphate synthase homology <SSS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
F;230-714/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-f1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T04103
R;Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T.
Plant Sci. 112, 207-217, 1995
A;Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene (A;Reference number: 215212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Dates: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999 C;Accession: T04062 #sequence_revision %; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, March 1999
                       A;Title: Analysis of CDNA clones encoding sucrose-phosphate synthase in relation in Reference number: 216874; MUID:97451773; PMID:9306694
A;Reference number: 216874; MUID:97451773; PMID:9306694
A;Recentering in the state of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 36; DB 2; Length 1083; 66.7%; Pred. No. 60; 1; Pred. 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 1081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: cultivar Columbia; BAC clone F28M11
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score 36; DB 2; Pred. No. 60; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1084 <SAK>
A;Cross-references: EMBL:D45890; PIDN:BAA08304.1
A;Experimental source: subsp. Japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-1083 <BEV>
A;Cross-references: EMBL:AL049487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.7
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:| |||:|
483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z15184
A; Accession: T04062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T04103
                                                                                                                                                                                                                                                                                                                                                                                                              C,Genetics:
A,Gene: sps2
C,Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ourses-phosphate synthase (EC 2.4.1.14) - maize
CiSpecies: Zea mays (maize)
CiSpecies: Zea mays (maize)
CiSpecies: Descriptor (maize)
CiAccession: J01329, PQ0260
CiAccession: J01329, PQ0260
Riworrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
Plant Cell 3, 113-1130, 1991
A;Title: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd
A;Reference number: J01329; MUID:92338837; PMID:1840396
                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-1049 «VML»
A; Cross-references: GB:U3175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A; Note: UDPglucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosylt
C; Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
C;Accession: JC4783
R;Valdez-Aharcon, J.J.; Perrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella Gene 170, 217-222, 1996
A;Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
A;Reference number: JC4783; MUID:96235138; PMID:8666248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: protein
A,Residues: 71-74;206-212;471-481;872-892 <WOR1>
C;Comment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-phosph
C;Comment: This enzyme is involved in the regulation of carbon partitioning in the leave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
A;Pathway: sucrose biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AiIntrons: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3; C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Pathway: sucrose biosynthesis
C; Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C; Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F; 178-666/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Species: Graterostigma plantagineum C;Species: Graterostigma plantagineum C;Date: 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: T09837 R;Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Residues: 1-1068 <WOR>
A, Residues: 1-1068 <WOR>
A, Cross-references: GB: M97550; NID: 9168625; PIDN: AAA33513.1; PID: 9168626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h Similarity 66.7%; Score 36; DB 2; Length 1049; Similarity 66.7%; Pred. No. 58; 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 1; Length 1068;
Pred. No. 59;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:| |||:|
436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:| |||:|
435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: PQ0260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: JQ1329
                                                                                                                                                                                                                                                                                         A;Accession: JC4783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: Sps1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

Ж. Ғ

ö

Ç

```
probable alkaline proteinase APE0263 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Accession: H72784
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak. R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak. S; Rakanabayasi, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA, Res. 6, 83-101, 1999
A;Ttle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop. A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72784
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 cKXW>
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79178.1; PID:g5103657
C;Genetics:
A;Gene: APE0263
C;Superfamily: subtilisin; subtilisin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 2; Length 440;
Pred. No. 35;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: clone R02D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 66.7%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 EVLPWGVDY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| |:|||
562 VLPVGIDYS 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Gene: CBSP: C53A5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: H87660
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
Bs; Laud, M.T.; DeBoy, R.T.; DeBoy, R.J.; DeBoy, R.J.; DeBoy, M.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUD:21173698; PMID:11259647
                                           A;Map posítion: 1
A;Map posítion: 1
A;Introns: 120/3; 200/2; 221/3; 452/3; 536/3; 536/3; 613/3; 634/3; 946/3; 989/2
A;Introns: 120/3; 200/2; 221/3; 452/3; 432/3; 536/3; 613/3; 634/3; 946/3; 989/2
C;Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase
E;196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.425 «MIL»
A;Cross-references: EMBL:281109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-433 <STO>
A;Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
C;Genetics:
A;Gene: CG322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein R10D12.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: D5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 (C;Accession: T24111 R;Percy, C. submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                          Length 1084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2; Length 433;
Pred. No. 34;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 425;
                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                       Score 36; DB 2;
Pred. No. 60;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 2;
Pred. No. 34;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:R10D12.10
A;Map position: 5
A;Introns: 23/3; 56/3; 113/3; 257/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone R10D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.8%;
54.5%;
                                                                                                                                                                                                    66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                 Query Match
Best Local Similarity 66.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 EVILPPGFDYS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 EQIVPGGLQY 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                             |:| |||:|
453 VIPPGMDFS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: Z19842
A;Accession: T24111
                                                                                                                                                                                                                                                                                                               3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Genetics:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                             셤
```

Gaps

```
A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2;
Aypothetical protein C53A5.2 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
Swidthare, B.
Swidthare, B.
Swidthare, B.
Sylvation: T20173
A;Reference number: Z1923
A;Reference number: Z1923
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1150 (WIL)
A;Cross-references: EMBL.Z81486; PIDN:CAB03994.1; GSPDB:GN00023; CESP:C53A5.2
A;Residues: 1-1150 (WIL)
A;Cross-references: EMBL.Data Library, August 1996
A;Recence number: Z19808
A;Recence number: Z19808
A;Recence number: Z19808
A;Recence to the EMBL Data Library, August 1996
A;Recence number: Z19808
A;Recence urber: Z19808
A;Recence to the EMBL Data Library, August 1996
A;Recence urber: Z1857
A;Residues: T23857
A;Residues: T21857
A;Residues: T21857
A;Residues: L1150 (WIL)
A;Cross-references EMBL.Z78015; PIDN:CAB01437.1; GSPDB:GN00023; CESP:C53A5.2
A;Cross-references: EMBL.Z78015; PIDN:CAB01437.1; GSPDB:GN00023; CESP:C53A5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.8%; Score 35; DB 2; Length 1150;
llarity 66.7%; Pred. No. 1e+02;
Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: December 22, 2003, 17:44:57 Job time : 9.06667 secs
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                     Run on:
```

December 22, 2003, 16:43:51 ; Search time 4.6 Seconds (without alignments) 112.455 Million cell updates/sec

US-09-909-164-12 54 1 EEVVPXGMDYS 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| SUMMAKIES | ID Description | CARB FUSNN O8rq86 fusobacteri | ď | 043802 | | 004933 | DROME P55824 dros | UMAN | P20423 oryz | P08248 | | P94283 | Q9£jk8 | Q8w4j9 | | Q58349 | 69A460 | | P08503 | 052250 | Cosen7 | 060344 | Q61851 | P18460 | 074377 | P27399 | IBCH 09kv29 | P15822 homo sa | ENLA | P20422 | Q92bc5 | ISMO Q8y6u8 | • |
|-----------|------------------|-------------------------------|------|--------|------|--------|-------------------|--------|-------------|--------|--------|--------|--------|--------|------|--------|--------|--------|--------|----------|--------|--------|--------|--------|--------|--------|-------------|----------------|--------|----------|--------|-------------|---|
| | DB I | - | 1 7 | . 8 | 1 8 | 7 | -1 | ж т | 1 | н П | 1 1 | 5 | ۳ ۲ | ۳ ٦ | 7 | ۲ ۲ | - | æ H | 1 | щ | я т | 7 E | 1 | 7 | 7 | 1 E | 7 | 1 2 | 1 E | <u>п</u> | r T | 1 1 | |
| | Length I | 1058 | 102 | 1049 | 1068 | 1081 | 2778 | 748 | 154 | 155 | 168 | 995 | 908 | 806 | 910 | 276 | 283 | 394 | 421 | 421 | 423 | 787 | 801 | 908 | 877 | 982 | 1401 | 2717 | 472 | 97 | 165 | 165 | |
| * | Query Match 1 | 70.4 | 66.7 | 66.7 | 66.7 | 66.7 | 64.8 | 63.9 | m | m | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | 61.1 | ٠ | • | 59.3 | 59.3 | |
| | Score | 38 | 36 | 36 | 36 | 36 | m | 34.5 | 34 | | 34 | 34 | 34 | 34 | | 33 | | | | 33 | | | | 33 | 33 | 33 | | 33 | 32.5 | 32 | 32 | | |
| | Result No. | | 7 | m | 4 | ស | φ | 7 | œ | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 53 | 30 | 31 | |

| P06190 salmonella Q9wzrl thermotoga Q04827 rattus norv P30279 home sapien P30280 mus musculu Q90459 brachydanio P50755 xenopus lae P49706 gallus gall P53782 xenopus lae P53169 gallus gall P53183 home sapien P24385 home sapien |
|---|
| ARAD SALTY HIS9 THEMA CGD2_RAT CGD2_RAT CGD2_MOUSE CGD1_BRARE CGD1_TRULA CGD2_CTICK CGD2_CTICK CGD2_TRULA CGD1_CTICK CGD3_TUMAN CGD1_TUMAN |
| аннянняння |
| 231 233 288 289 291 291 292 292 |
| $\begin{array}{cccccccccccccccccccccccccccccccccccc$ |
| |
| ₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩ |

ALIGNMENTS

7 QVVPSGINYS 16

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
R PRINTS; PRO0098; CPSASE.

R TIGREAMS: TIGRO1369; CPSASE.

R PROSITE; PS00866; CPSASE.1; 2.

DR PROSITE; PS00867; CPSASE.1; 2.

DR PROSITE; PS00867; CPSASE.2; 2.

KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Liga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92188538; PubMed=1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas the morphism of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonus plants."; Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
ATP (POTENTIAL).
ATP ANGANNES I (BY SIMILARITY).
MANGANESE I AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 1058; Pred. No. 9.1; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 2; ive 3; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 MANGANESE 3 (BY SIMILARITY).
32 MANGANESE 3 (BY SIMILARITY).
117451 MW, ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l protein. Table MW; A40BCF1B0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A42452; A42452.
InterPro; IPR002621; Gemini mov.
Pfam; PF01708; Gemini mov; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 60.0
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses, ssDNA vi)
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                            547
3302
284
298
300
820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y11K TYDVA
P31619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIIK TYDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- PATHWAY: Sucrose synthesis.
-1- SUBUNIT: Homodimer or homotetramer (By similarity).
-1- PTH : PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                               Gaps
                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucross-phosphate synthase (BC 2.4.1.14)
(UDP-glucose-phosphate glucosyltransferase).
(UDP-glucose-phosphate glucosyltransferase).
Srastiva (Rice).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                      "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Score 36; DB 1; Length 1049; 66.7%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            775 779 POLY-ARG.
1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
                                                                                                                                                                                                                                                                        Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orangene, V. 1970.2, 1970. Lrans 1.
Pfam; PR001296; Glyco_trans 1.
Pfam; Pr0034; Glycos transf 1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN 22 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1068 AA.
                             1049 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLU
                                                                                                                                                                                                                                          STRAIN=cv. Indica-IR36; TISSUE=Leaf;
MEDLINE=96235138; PubMed=8666248;
                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPS MAIZE STANDARD;
P31927;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U33175; AAC49379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; JC4783; JC4783.
                                                                                                                                                                                                                                                                                         Herrera-Estrella L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gramene; Q43802;
                                                                                                                                                                                              NCBI_TaxID=4530;
                          SPS_ORYSA
Q43802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
SPS_MAIZE
RESULT 3
SPS_ORYSA
                               a y a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

ö

2 EVVPXGMDYS 11

ò

```
Asteridae; lamilds; Lamiales; Lamiales incertae sedis; Torenieae;
                 Craterostigma.
NCBL_TaxID=4153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: SUCTOBE SYNCHESIS.
SUBUNIT: HOMODIMER OR HOMOTETRAMER.
DEVELOPMENTAL STAGE: GERMINATING SEEDS OR MATURE LEAVES.
PTM: PHOSPHORYLATED. HOMEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR
                                                                                                                                                                        STRAIN=CV. PIONEER 3184; TISSUE=Leaf;
MEDLINE=233887; PubMed=1840396;
Worrell A.C., Bruneau J.-M., Summerfelt K., Boersig M., Voelker T.A.;
"Expression of a maize sucrose phosphate synthase in tomato alters
leaf carbohydrate partitioning.";
                                                                                                                                                                                                                                                         FUNCTION: INVOLVED IN THE REGULATION OF CAREON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREPORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                           Eukaryota, Vizidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craterostigma plantagineum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (RC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase 2).
                                                                                                                                                                                                                                                                                                                          BUCIOSE 6-Phosphate.
ENZYME REGILATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND
MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 36; DB 1; Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR001296; Glyco_trans_1.
Pro0534; Glycos transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN 25 31
PoLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1081 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 24;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M97550; AAA33513.1; -. PIR; JQ1329; JQ1329.
                                                                                                                                                                                                                                               Cell 3:1121-1130(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435 VIPPGMDPS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                              ENZYME FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                  NCBI_TaxID=4577;
                                                                 Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MaizeDB; 25294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPS2_CRAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPS2_CRAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
ઠે
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Ruropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAR DROWE STANDARD; PRT; 2778 AA.

PASE DROWE STANDARD; PRT; 2778 AA.

PASE DROWE STANDARD;

TO 1-00V-1997 (Rel. 35, Created)

TO 28-FEB-2003 (Rel. 41, Last sequence update)

TO 28-FEB-2003 (Rel. 41, Last sequence representation update)

TO 28-FEB-2003 (Rel. 41, Last sequence update)

TO 28-FEB-2003 (Rel. 41, Last sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97411773; PubMed=9306694;
MEDLINE-97411773; PubMed=9306694;
MEDLINE-97411773; PubMed=9306694;
MEDLINE-97411773; PubMed=9306694;

"Analyais of cDNA clones encoding sucrose-phosphate synthase in relation to sugar interconversions associated with dehydration in the resurrection plant Craterosetigma plantagineum Hochst.";
Plant Physiol. 115:113-121(1997).

--- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLAYS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREPORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.

--- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PinterPro; IPR001296; Glyco trang 1.
Pfam; PF00534; Glycoe_trangf_1; T.
Trangferage; Glycosyltrangferage; Phosphorylation; Multigene family.
DOMAIN 245 248 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUB SPECIFICITY. TISSUB-EBye imaginal disk;
MEDLINE-93202020: Pubmed=1255747;
Fischer-Vize J.A., Rubin G.M., Lehmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 36; DB 1; Length 1081; 66.7%; Pred. No. 24; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y11795; CAA72491.1; -. PIR; T09837; T09837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.77,
Annual 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMDYS 11
```

```
The fact facets game is required for Drosophila eye and embryo embryo and embryo emb
```

```
A GO;
A GO;
A InterPro; IPR0013>*,
DR PEAM; PF00443; UCH; 1.
DR PROSITE; PS00973; UCH=2; 1.
DR PROSITE; UCH=
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Ewropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PlyBase; FBgn0005632; faf.

60, 60:0005737; C:Cytoplasm; IDA.

GO; 00:0007349; P:Cetluarization; IMP.

GO; 00:0007349; P:Cetluarization; IMP.

GO; 00:0008583; P:mystery cell fate differentiation (sensu Dr. . .; IMP.

GO; 00:0007097; P:nuclear migration; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                 Isold=P55824-3; Sequence=VSP 005269;
-1- TISSUR SPECIFICITY: EYE DISKS AND OVARIES.
-1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-1- SIMILARITY: Belongs to peptidase family C19.
COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR
                                                   -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                   IsoId=P55824-2; Sequence=VSP_005270;
                                                                                                                                                                                                                                IsoId=P55824-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L04959; AAF01345.1; -.
EMBL; L04958; AAF01346.1; -.
EMBL; L04960; AAF01347.1; -.
EMBL; L04960; AAF01348.1; -.
EMBL; AE003779; AAF57198.1; -.
EMBL; AE003779; AAN14291.1; -.
EMBL; AF145677; AAD38652.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : | | | : |
1394 EVIVPDGQDFS 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EBVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF145677; AMEROPS; C19.007;
                                                                                                                                                                                     1 BOFOTMB;
                                                                                                                                                                                                                                                           Name=2;
                                                                                                                                                                                                                                                                                                            Name=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
Š
```

RESULT 7
KHL1_HUMAN

ï

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=20277482; PubMed=10819331;
MEDLINE=20277482; PubMed=10819331;
Magase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XVII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM, 605332; -...

GO: GO:0003779; F:actin binding activity; NAS.

GO: GO:000379; F:actin cytoskeleton organization and biogenesis; NAS.

InterPro; IPR000510; BTB POZ.

InterPro; IPR00652; Kelch_rep.

Pfam; PP00541; Kelch_rep.

Pfam; PP01344; Kelch; 6.

SNART; SM00525; BTB; 1.

SWART; SM00512; Relch; 6.

PROSITE; PS50097; BTB; 1.

Cytoskeleton; Actin-binding; Kelch_repeat; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!-EUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
THE BRAIN CELLS.
                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=20347694; PubMed=10888605;
Krob M.D., Nemes J.P., Benzow K.A.;
trob M.D., Nemes J.P., Benzow K.A.;
transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI).";
Hum. Mol. Genet. 9:1543-1551(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C11C43D8282F9FF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- TISSUE SPECIFICITY: Highly expressed in brain.
-i- SIMILARITY: Contains 1 BTB/POZ domain.
-i- SIMILARITY: Contains 6 Kelch repeats.
KHL1 HUMAN STANDARD; PRT; 748 AA. QSNR64; QSH4X4; QSNR65; QSP238; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Kelch-like protein 1. KALH1 OR KIAA1490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF252283; AAF81719.1; -.
EMBL, AF252279; AAF81716.1; -.
EMBL, AB040923; BAA96014.1; ALT_INIT.
EMBL, AL353738; CAC16128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82680 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 179-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:6352; KLHL1.
MIM; 605332; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
279
506
553
600
647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555
601
649
701
748 AA;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
```

DB 1; Length 748;

Score 34.5;

63.9%;

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               Gaps
                                                                                                                                                                                                                                                                                                                    Molecular cloning and characterization of plastocyanin precursor in
                                                                                                                                                                                                                    Bukaryota, Viridipiantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD001235; Copper blue; 1.
PROSITE; PS00196; COPPER BLUE; 1.
Chloroplast; Blectron transport; Copper; Thylakoid; Membrane;
Transit peptide.
157 CHLOROPIAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 154;
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
4; E45725D25B5F400D CRC64;
                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLASTOCYANIN.
PLASTOCYANIN-LIKE.
                                                                                                                                P20423; Q95BBB;
01-FEB-1991 (Rel. 17, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
PERB-2003 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
                                                                                                                         154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB :
Pred. No. 8.1;
              1; Mismatches
 80.0%; Pred. No. 34;
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gramene; P20423; -.
InterPro; IPR000923; BlueCu 1.
InterPro; IPR001235; Copper_blue.
Pfam; PR00127; copper_blud; 1.
PRINTS; PR00156; COPPERBLUE.
                                                                                                                                                                                                                                                                                            STRAIN=cv. Ilpoom; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF093636; AAC78108.1; -. HSSP; P00289; 2PCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15577 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.0%;
54.5%;
            Conservative
                                                                                                                        STANDARD:
                                                 ||||| |||:
127 BEVVP-GMDF 135
                                     1 REVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
154
154
139
142
                                                                                                                                                                                                           Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
154 AA;
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 58-154
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gramene; P20423;
                                                                                                                        PLAS ORYSA
                                                                                                                                                                                                                                                                                                           Lee J.-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                    rice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                           PLAS_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                     à
                                                         셤
```

Gaps

ö

Indels

<u>.</u> ج

Matches

RESULT

셤

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Malpighiales, Salicaceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R PISP, D00299, 1PLC.
R HSSP, P00299, 1PLC.
R InterPro; IPR000923; BlueCu 1.
R InterPro; IPR001235; Copper_blue.
R PRIMTS; PR00127; Copper_blue.
DR PROSTIR; PS00156; COPPER BLUE; 1.
DR PROSTIR; PS00196; COPPER BLUE; 1.
FT TRANSIT 1 69 PLASTOCYANIN B.
DELASTOCYANIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. Italica;
Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
"Complete amino acid sequence of poplar plastocyanin b.";
PEBS Lett. 226:17-22(1987).
-1- FUNCTION: Participates in electron transfer between P700 and tortochrome be-f complex in photosystem I.
-1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
-1- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS AND B.
-1- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. Italica, TISSUB=Leaf,
Reichert J., Jenzelewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                             01-0CT-1989 (Rel. 12, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                            168 AA
      Pred. No. 8.2;
                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Plastocyanin B, chloroplast precursor.
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Populus nigra (Lombardy poplar).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z50186; CAA90565.1; -.
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                       6; Conservative
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                 101 EDAVPSGVDVS 111
                                                                                          1 BEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S00210; S00210.
PIR; S58208; S58208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106
153
156
156
161
168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 70-168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                            PLAT POPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                 P11970;
                                                                                                                                                                                                                                   RESULT 10
PLAT POPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                    Matches
                                                                                                                                                                                                                                                                                                                       SOTTE THE TENT TO 
                                                                                          8
                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nielsen P., Gausing K.;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene promoter region.";
Promoter region.";
Eur. J. Biochem. 217:97-104 (1993).
-!- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.
-!- SUBCELLILLAR LOCATION: LOCASELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nielsen O.S., Gausing K.;
The precursor of barley plastocyanin: sequence of cDNA clones and
gene expression in different tissues.";
FEBS Lett. 225:159-162(1987).
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD001235; Copper blue; 1.
PROSITE; PS00196; COPPER BLUE; 1.
Chloroplast; Blectron transport; Copper; Thylakoid; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 155;
         Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPER (BY SIMILARITY).

-> N (IN CV. NK 1558).

DAA7EABE5F6F4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY)
COPPER (BY SIMILARITY)
      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1;
                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-BEB-2003 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHLOROPLAST.
PLASTOCYANIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y00704; CAA68696.1; -.
EMBL; 228347; CAB2201.1; -.
EMBL; 23825; S3825.
HSSP; P00289; 2PCF.
InterPro; IPR00023; BlueCu_1.
InterPro; IPR001235; Copper_blue.
Pfam, PF00127; copper_blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. NK 1558;
MEDLINE=94039081; PubMed=8223592;
      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00156; COPPERBLUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15709
         Conservative
                                                                                                                      EDAVPSGVDVS 110
                                                                                                                                                                                                                                                                    STANDARD;
                                                               1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
155
155
155
140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
148
120
155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transit peptide.
TRANSIT 1
CHAIN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bomi;
      . 9
                                                                                                                                                                                                                                                                 PLAS HORVU
P08248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
METAL
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                      PLAS HORVU
```

SOURCE STATES AND DESCRIPTION OF STATES AND DESCRIPTION OF STATES AND SOURCE STATES AND DESCRIPTION OF STATES AND DESCRIPT

```
ö
                                                     Gaps
                                                     ö
                       63.0%; Score 34; DB 1; Length 168; 54.5%; Pred. No. 8.9;
                                                     Indels
F20DA6EA2038AEEA CRC64;
                                                   2; Mismatches
```

a

```
용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
tRNA ligase beta chain) (PheRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIR-ATCC 35210 / B31;
MEDLINE-98065943; Pubmed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03484; B5; 1.
TIGRPAMs; TIGR00471; pheT arch; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barbour A.G., Hinnebusch J.;
Phenylalanyl-ErRMA synthetase genes (alpha and beta subunits) and
thioredoxin reductase gene of Borrelia burgdorferi.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

    similarity).
    SUBCELLULAR LOCATION: Cytoplasmic.
    SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN FAMILY. SUBFAMILY 2.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:580-586(1997).
-!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP
diphosphate + L-phenylalanyl-tRNA(Phe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Tetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; Score 34; DB 1; Length 566; 85.7%; Pred. No. 32; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                                    566 AA.
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00284; -; 1.
InterPro; IPR005147; B5.
InterPro; IPR004531; PheT_arch.
                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U82978; AAB41019.1; -.
EMBL; AE001153; AAC66870.1; -
PIR; A70164; A70164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
                                                                     112 EDAVPSGVDVS 122
                                                                                                                                                                                                                                                STANDARD;
1 EBVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome
SEOUENCE 566 AA
                                                                                                                                                                                                                                             SYFB BORBU P94283;
                                                                                                                                                                                                                SYFB_
```

ö

Gaps

; 0

Conservative

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaseb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. Columbia;
A Seki M., Ilda K., Satou M., Sakurai T., Akiyama K., Ishida J.,
A Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
A Hayashizaki Y., Shinozaki K.;
T "Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
C -!- FUNCTION: Pocential disease resistance protein.
C -- FUNCTION: Pocential disease resistance protein.
C -- FUNCTION: Pocential disease resistance protein.
C -- BALDAGEN TO ELER repeats probably act as specificity determinant of pathogen recognition (By similarity).
C --- SIMILARITY: Connains 3 leucine-rich (LRR) repeats.
C --- SIMILARITY: Connains 1 NB-ARC domain.
C --- DATABASE: NAME-NIB-LRRS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE=Punctional and comparative genomics of disease resistance gene
                                                                                                                                                                          15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable disease resistance RPP8-like protein 4.

RPP8H4 OR AT5G48620 OR K15N18.9.

Arabidopsis thaliana (Mouse-ear cress).

Rukaryota, Viridiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                        STRAIN-cv. Columbia;
MEDLINE-99087489; PubMed-9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones."; DNA Res. 5:297-308(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interro; servos...
Pfam; PR00560; LRR; 2.
Pfam; PR0031; NB-ARC; 1.
PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
A5 LBUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.
(POTENTIAL)
                                                                                                                           908 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000767; Disease resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRR 1.
LRR 2.
LRR 3.
ATP (PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB015468; BAB10695.1; -. 
EMBL; AK117163; BAC41841.1; -.
                                                                                                                                                            (Rel. 42, Created)
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
459
599
623
867
                               169 VPPGMDY 175
4 VPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homologs;
                                                                                                                                                            15-SEP-2003
                                                                                                                         R8L4 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                    rabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
REPEAT
REPEAT
NP_BIND
```

```
ô
                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. Columbia, and cv. Landsberg erecta;
STRAIN-cv. Columbia, and cv. Landsberg erecta;
MEDLINE=99030193; Pubbed=9811794;
MCDowell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
Holub B.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPPB locus of Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cooley M.B., Pathirana S., Wu H.J., Kachroo P., Klessig D.F.; "Members of the Arabidopsis HRT/RPP8 family of resistance genes confer resistance to both viral and comycete pathogens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                   QBW4J9; QBGMG5; Q9M5A1; Q9ZSY3; Q9ZSY4; 15-SEP-2003 (Rel. 42, Created) 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last amount and pare blasease resistance protein RPP8 (Resistance to Peronospora parasitica protein 8).
                                                                                                                                                                                                                  RPPB OR HRT OR AT5G43470 OR MWF20.19.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                               Gaps
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 AND RPP8-3, AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=cv. Columbia;
STRAIN=Ex. Columbia;
SECORDINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length CDNA clones (RAFLs) sequenced by SSP consortium (Salk/Stanford/PGEC) "; submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                               ö
                      63.0%; Score 34; DB 1; Length 908; 60.0%; Pred. No. 53; ive 2; Mismatches 2; Indels
908 AA; 104448 MW; 3111991B17239693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Di-17;
MEDLINE=20271766; PubMed=10810142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH TIP.
MEDLINE=20496823; PubMed=11041886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                        lant Cell 10:1861-1874(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Cell 12:663-676(2000).
           Ouery Match
Best Local Similarity 60...
Best Conservative
                                                                                              883 EKLVPGGEDY 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clones.";
DNA Res. 7:31-63(2000)
                                                                      1 EEVVPXGMDY 10
 SEQUENCE
                                                                                                                                              RPP8 ARATH
                                                                                                                               RESULT 13
 g
                                                                                                                                                                    ઠે
                                                                                              ద
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q8W4J9-2; Sequence=VSP_007171, VSP_007172;
Note=Has been shown to exist only in cv. Columbia so far;
-!- DOMAIN: The LRR repeats probably act as specificity determinant of
                                                                                                             the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. The interaction with TIP (TCV-interacting protein) may be essential for the recognition of the avirulence proteins, and the triggering of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen recognition.

POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and cv. Columbia are probably due to an unequal crossing-over between the highly related RPPs and RPHBA genes present in cv. Landsberg erecta. Such variations probably modify the specificity of
Ren T., Qu F., Morris T.J.;
"HRT gene function requires interaction between a NAC protein and viral capsid protein to confer resistance to turnip crinkle virus."; plant Cell 12:1917-1926 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRR 1.
LRR 2.
ATP (POTENTIAL).
WYMLLTSRNEGVGIH -> BLLWYIHEALFLLINS (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant defense; ATP-binding; Repeat; Leucine-rich repeat; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /PTId=VSP_007171.
Missing (in isoform 2).
/FTId=VSP_007172.
                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Interacts with the NAC protein TIP.-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q8W4J9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homologs;
WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF089711; AAC78631.1; -. EMBL; AF244174; AAF36987.1; -. EMBL; AB025638; BAA97426.1; -. EMBL; AY062514; AAA132592.1; -. EMBL; AX118862; BAC43449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF089710; AAC83165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00364; DISEASERSIST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           867
199
308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00560; LRR; 2.
Pfam; PF00931; NB-ARC;
                                                                                                                                                                                                                                                                                                                  defense response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
REPEAT
REPEAT
NP BIND
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
```

|::|| | || 883 EKLVPGGEDY 892

```
SOUTH THE TOUR COUNTY TO THE TENT OF THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
    cv. Landsberg erecta).
                                            Landaberg erecta).

GKGV -> EKGI (in cv. Landaberg erecta).

C -> R (in cv. Landaberg erecta).

C -> D (in cv. Landaberg erecta).

F -> L (in cv. Di-17).

G -> Q (in cv. Di-17).

G -> C (in cv. Di-17).

G -> C (in cv. Di-17).

R -> T (in cv. Di-17).

R -> T (in cv. Di-17).

R -> F (in cv. Di-17).

A -> T (in cv. Di-17).

A -> Y (in cv. Di-17).

A -> Y (in cv. Di-17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erecta).

YEAK -> FLAG (in cv. Landsberg erecta).

NLRVDT -> DLSVHE (in cv. Di-17).

RVDTB -> SVNNK (in cv. Landsberg erecta).

Q -> E (in cv. Di-17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T -> I (in cv. Di-17).
S -> R (in cv. Di-17).
S -> R (in cv. Di-17).
H -> Q (in cv. Di-17).
I -> L (in cv. Landsberg erecta).
KNKT -> KNNA (in cv. Di-17).
K -> N (in cv. Landsberg erecta).
FRPEEDYW -> WDEDFG (in cv. Landsberg
                                                                                                                                                                                                                                                                                                                                    erecta).

W -> C (in cv. Di-17 and cv. Landsberg erecta).

erecta).

erecta).

N -> F (in cv. Di-17 and cv. Landsberg erecta).

N -> F (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A -> V (in cv. Landsberg erects).
B -> Q (in cv. Landsberg erects).
DNYLSWQ -> NKYLRVH (in cv. Di-17).
DN -> NR (in cv. Landsberg erects).
WQ -> SH (in cv. Landsberg erects).
Y -> N (in cv. Landsberg erects).
I -> K (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRF -> SRFK (in cv. Di-17).
Y -> F (in cv. Di-17).
Y -> Y (in cv. Landsberg erecta).
C -> S (in cv. Landsberg cv. Landsberg
                                                                                                                                                                                                                                                                                                        erecta). F \rightarrow S (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erecta).
C -> S (in cv. Di-17 and cv. Landsberg
erecta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YL -> HI (in cv. Di-17).
Missing (in cv. Di-17).
M -> K (in cv. Landsberg erecta).
YLY -> FLF (in cv. Landsberg erecta).
YGY -> FR (in cv. Landsberg erecta).
                                                                                                                                                                                                                                                                                                                                                                                                                                      erecta).
DSEISTYSLFY -> YSKISAYDLFN (in cv.
   IDGQL -> VDEQI (in cv. Landsberg G -> E (in cv. Di-17).
SGK -> RGE (in cv. Di-17 and cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> H (in cv. Landsberg erecta).
-> Q (in cv. Di-17).
-> G (in cv. Di-17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Landsberg erecta).
EISTYS -> KITTQE (in cv. Di-17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB :
Pred. No. 53;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erecta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erecta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481
486
489
514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450
460
486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5528
5528
5542
5553
5550
                                                               387
                                                                                                                                                                                                                                                                                                                                                       399
                                                                                                                                                                                                                                                                                                                                                                                        426
                                                                                                                                                                                                                                                                                                                                                                                                                      429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                88
100
1121
1121
1133
1138
1177
1177
253
257
265
265
270
                                                                                                                                                                                                                                                                                                                                                       399
                                                                                                                                                                                                                                                                                                                                                                                      426
                                                                                                                                                                                                                                                                                                                       387
                                                                                                                                                                                                                                                                                                                                                                                                                      429
                                                                                                                                                                                                                                                                                                                                                                                                                                                    436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
                                                                                                                            VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
VARIANT
VARIANT
                                                               VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
```

```
The Arabidopsis.

1. Arabidopsis.

1. FUNCTION: Disease resistance protein. Resistance proteins guard

1. FUNCTION: Disease resistance protein. Resistance proteins guard

2. The plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein.

2. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. In contrast to RPB9, it does not specifically recognize the Emco5 avirulence protein from Peronospora parasitica.

2. MISCELLANEOUS: In cv. Columbia and cv. Di-17, this protein is not present due to an unequal crossing over between the RPP8 and RP8HA present due to an unequal crossing over between the RPP8 and RP8HA creates a unique RPP8 gene.

2. SIMILARITY: Belongs to the disease resistance NB-LRR family.

2. SIMILARITY: Contains 1 NB-ARC domain.

2. SIMILARITY: Contains 1 NB-ARC domain.

2. NATABASE: NAME-NIB-LRRS;

2. NATABASE: NAME-NIB-LRRS;

3. NATE-Functional and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND FUNCTION.
STRAIN=cv. Landsberg erects;
MEDLINE=99030193; PubMed=9811794;
MCDowell J.M., Dhandsydham M., Long T.A., Aarts M.G.M., Goff S.,
Holub B.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the
                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.0%; Score 34; DB 1; Length 910; 60.0%; Pred. No. 53; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       625 LRR 1.
869 LRR 2.
199 ATP (POTENTIAL).
105263 MW; SBIBSP6SA19A12EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WWW=http://niblrs.ucdavis.edu".
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN 10 45 LEUCINE-ZIPPER.
                                                                                                   15-SBP-2003 (Rel. 42, Created)
15-SBP-2003 (Rel. 42, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Disease resistance protein RPH8A (RPP8 homolog A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
16.OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NB-ARC.
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein MJ0939.
MJ0939.
Methanococcus jannaschii.
                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   885 KKLVPGGEDY 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 REVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 1
910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homologs;
                                              RP8H ARATH
P59584,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y939 METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
RESULT 14
RP8H ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88888888
```

Conservative

ö

Gaps

ö

2; Indels

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                  STRAINS—JAL-1 / DSW 2661 / ATCC 43067;
STRAINS—JAL-1 / DSW 2661 / ATCC 43067;
STRAINS—JAL-1 / DSW 2661 / ATCC 43067;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Butt C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlawage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkmess B.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 1; Length 276;
Pred. No. 24;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; MJ0939; -.
Pfam; PF03692; UPF0153; 1.
Hypothetical protein; Complete proteome.
SRQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;
Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.1%; 645.5%; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U67537; AAB98946.1; -. PIR; C64417; C64417.
                                                                                                                                                                                                                                                                                                                                                            jannaschii.";
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:: ||::|
141 EEIIENGMEHS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EEVVPXGMDYS 11
                                                  NCBI_TaxID=2190;
  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
```

Search completed: December 22, 2003, 17:42:26 Job time : 4.6 secs

```
RESULT 1
                                                                                                                                                                                                                                                                                 012479
                                                                                                                                                                                                                                                                                                  Q8esv7 oceanobacil
030260 archaeoglob
08dih0 synechococc
022081 citrus unsh
022096 citrus unsh
08c68 arabidopsis
09c9t7 arabidopsis
09c9t7 arabidopsis
09c9t0 arabidopsis
09sn30 arabidopsis
043010 oryza sativ
08s064 oryza sativ
08spa8 closeridium
062367 rhizobium t
08st43 rhizobium e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q12479 saccharomyc
                                             December 22, 2003, 17:27:26; Search time 25.2 Seconds (without alignments) 112.642 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                        830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                        830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9GQ04
Q8XPA8
O52367
Q8KL43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBESV7
030260
QBDIH0
022081
022096
QBW568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P93782
Q9SN30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q43010
Q8S064
                                                                                                                                                                                                                                                                                                                         sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                      sp_bacteria:*
sp_bacteria:*
sp_fungl:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     012479
                                                                                                                                                                                                                                                                                                                                                            sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                       seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
10
10
10
10
10
10
                                                                               US-09-909-164-12
54
                                                                                              1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length DB
                                                                                                                                                                                                                                                                                                                 sp plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1047
1083
1084
1100
219
                                                                                                                                                                                                                                SPTREMBL
                                                                                                               BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Storing table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                               OM protein
                                                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                                                                                                                                 Database :
                                                                                               Sequence:
                                                                                                                                        Searched:
                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š.
```

| Q9xvk4 caenorhabdi | Q9a382 caulobacter | Q9yfi3 aeropyrum p | | Q8xz15 ralstonia s | Q946j7 andrographi | | | 017704 caenorhabdi | O52673 escherichia | | O27146 methanobact | Q98k29 rhizobium l | Q8tbj7 homo sapien | Q9vsy8 drosophila | Q8r915 thermoanaer | Q8e519 streptococc | Q8dzw9 streptococc | Q8gp33 lactobacill | Q8u7j0 agrobacteri | | O29920 archaeoglob | O29451 archaeoglob | | Q8tff4 trichoderma | Q8r8z2 thermoanaer | Q9cin1 lactococcus | | |
|--------------------|--------------------|--------------------|--------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-----------|--------------------|--------------------|-----------|--------------------|--------------------|--------------------|-----------|-----------|
| 5 Q9XVK4 | .6 Q9A3B2 | 17 Q9YFI3 | 052680 | STZX8Ö 9 | .0 0946J7 | . Q95P46 | 6 Q9U6A3 | 017704 | 052673 | 052666 | .7 027146 | .6 Q98K29 | Q8TBJ7 | 9 Q9VSYB | .6 Q8R9L5 | .6 Q8E5L9 | .6 Q8DZW9 | Q8GP33 | .6 Q8U7J0 | .7 Q9YET8 | .7 029920 | .7 029451 | .6 Q98FX1 | Q8TFF4 | .6 QBR8Z2 | .6 Q9CIN1 | .6 Q9JZP8 | .6 Q8G3J2 |
| 425 5 | 433 1 | 440 1 | 511 2 | 517 1 | 595 1 | 745 5 | 1031 5 | 1150 5 | 1410 2 | 1420 2 | 1474 1 | 1828 1 | 748 4 | 143 5 | 215 | 222 1 | 222 | 284 2 | 290 1 | 296 1 | 357 1 | 366 1 | 387 1 | 543 3 | 558 1 | 565 1 | 587 1 | 671 1 |
| 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 63.9 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 |
| 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 34.5 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 |
| 11 | 18 | 19 | 50 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

```
MEDLINE=94019918; PubMed=8413243;
Dumont M.B., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy
                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Bukarycta; Mugi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaces;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CYC2 encodes a factor involved in mitochondrial import of yeast
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                           Last sequence update)
Last annotation update)
  PRT; 156 AA.
                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome c.";
Mol. Cell. Biol. 13:6442-6451(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-FY1679;
MEDLINE-94169519; PubMed=7764548;
                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21, ORF YOR013W.
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherman F.;
Q12479
Q12479;
                                                                                                                                              YOR013W
```

. :

Gaps

ö

ò g

```
Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.T., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocsayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Rujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Citrus unshiu (Satsuma orange).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=2225144; PubMed=12240834;

Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto & Makamara Y., Kaneko T., Sato S., Ikeuchi M., Kishida Y., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Tompitete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";

DNA Res. 9:123-130(2002).

EMBL, PADOS374; BAC09170.1; -. Complete proteone.

SEQUENCE 1044 AA; 113205 WW; 0089C13F0F636D2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 1044;
                                                                                                                                                                                                                                                                                                                                                 70.4%; Score 38; DB 17; Length 363; 54.5%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria, Cyanobacteria, Chroococcales, Synechococcus.
                                                                                                                                                                                                                                           InterPro; IPR002103; Bac_luciferase.
Pfam; PF00296; bac_luciferase; 1.
Hypothetical protein; Complete proteome.
BRQUENCE 363 AA; 41736 MW; 0E976EAB788F4803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Multidrug efflux transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1044 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.4%; Score 38; DB 63.6%; Pred. No. 53; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sucrose-phosphate synthase (Fragment). CITSPS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                        EMBL; AR001109; AAB91255.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.6%;
                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :|| |:||
120 RNIVPYGIDFS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          843 REVLPNGIGYS 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                               1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Cyanoba
NCBI_TaxID=32046;
                                                                                                                                                                                                                               TIGR; AF2411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BP-1;
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLL1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                022081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           022081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Онідеб
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
Q8DIH0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           022081
      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSSEPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=HTEB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlawage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
  Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;

"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";

Biosci. Biotechnol. Blochem. 58:391-395(1994).

EMBL; Z74920; CAA99201.1; -.

EMBL; X77331; CAA60762.1; -.

SGD; S0005539; YOR013W.

SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.4%; Score 38; DB 16; Length 319; 60.0%; Pred. No. 14; ive 3; Mismatches 1; Indel8
                                                                                                                                                                                     74.1%; Score 40; DB 3; Length 156; 77.8%; Pred. No. 2.3; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 30:3927-3935 (2002).
EMBL; AP004594; BAC12465.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 319 AA; 35617 MW; 3BDAB4BF13B79E37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Buryarchāeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein AF2411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical conserved protein. OB0509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.08;
                                                                                                                                                                Query Match
Best Local Similarity 77.00.,
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::|| |:||
189 EQLVPHGIDY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EBVVPXGMDY 10
                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                            EVVPXGMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             environments."
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8ESV7;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            030260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF2411.
                                                                                                                                                                                                                                                                                                                                                                                                                Q8ESV7
                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         030260
                                                                                                                                                                                                                                                                                                                                                                                           Q8ESV7
```

ö

Gaps

ö

ò g

```
Cheuk R., Chen H., Kim C.J., Koeeema B., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                              Arabidopais thallana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 10; Length 452;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rcker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                   01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
1-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Atlg/3750/F25F22 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 50.6 kDa protein.
                                                                                                                                                                                                   452 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 EEDVPSAMDY 219
         1:| |||:|
234 VIPPGMDFS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 REVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eurosids II; Bra:
NCBI_TaxID=3702;
                                                                                                                                                                                             08W568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9C9T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                            셤
                                                                                                                                                                                                                            DDR REPARANCE OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. Miyagawa-Wase; TISSUE-Juice sacs and segment epidermis; Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; Tofferential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; Plant Sci. 140:169-178(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

TISSUE-Juice sacs and segment epidermis;

Komataw A., Takanokura Y., Morguchi T., Omura M., Akihama T.;

Komataw A., Takanokura Y., Morguchi T., Omura M., Akihama T.;

"Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (citrus unshiu Marc.).";

Plant Sci. 140:169-178[1999).

EMBL: AB006660; BAA22071.1;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Sapindales; Rutaceae; Citrus.
NCBL_TaxID=55188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                       STRAIN=cv. Miyagawa-Wase, TISSUE-Juice sacs and segment epidermis, MEDLINE-56439842; PubMed=6842155; Komatsu A., Takannokura Y., Omura M., Akihama T.; "Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Juice sacs and segment epidermis;
MEDLINE-96439842; PubMed=8842155;
KOmatsu A., Takanokura Y., Omura M., Akihama T.;
"Cloning and molecular analysis of CDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Score 36; DB 10; Length 341; 66.7%; Pred. No. 40; 1: Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 66.7%; Score 36; DB 10; Length 348; Best Local Similarity 66.7%; Pred. No. 41; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 AA; 38136 MW; 61417A69C4560777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 AA; 38556 MW; EEIC21EBA6FF5C5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or-be-2001 (ilembrier. 19, base anno
Sucrose-phosphate synthase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                     Marc.).";
Mol. Gen. Genet. 252:346-351(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Gen. Genet. 252:346-351(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Citrus unshiu (Satsuma orange)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| |||:|
228 VIPPGMDFS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=55188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marc.).";
                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

022096

RESULT 6 022096

Matches

ሯ a

ö

Gaps

thaliana.

SEQUENCE

Query Match

Matches

```
"Structure and RPLP mapping of a rice sucrose phosphate synthase (SPS) gene that is specifically expressed in the source organ."; Plant Sci. 112:207-217(1995).
                                                                                                                                                                                                                                                                                                 Arabidopais thaliana (Mouse-ear cress).

Rukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rossidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
BEVAN M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. japonica;
Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
Pujimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 36; DB 10; Length 10
66.7%; Pred. No. 1.5e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, D45890 BAA08304.1; -. Gramene; Q43010; -. InterPro; IPR001296; Glyco_trans_1. InterPro; IPR001595; Glyco_trans_1. InterPro; IPR001557; L.LDH. From; PF00054; Glycos_transf_1; 1. PR00SITE; PS00064; L.LDH; 1. SEQUENCE 1084 AA; 119417 MW; 4D0D79AFEDD2F92B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1083 AA; 122688 MW; BFC126FCA2137BB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KU Arabidopsis sequencing project;
Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL049487; CAB397641; -.
INLA1916; CAB397641; -.
InterPro; IPR001296; Glyco_trans_1.
Pfam; PR00534; Glycos_trans_1.
Glycosyltransferase; Transferase.
SEQUENCE 1083 AA; 122688 MW; EFC126FCA2137BB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU Arabidopsis sequencing project;
Submitted (SRP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Sucrose-phosphate synthase-like protein (BC 2.4.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sucrose phosphate synthase.
                                                                                                           PRT; 1083 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1084 AA
                                                                                                                                                                       (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:| |||:|
483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                                                                                                                                                       01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                Q9SN30;
                                                                                                   Q95N30
                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        043010
                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCOCCOS ON THE STANT OF STANTANT OF STANT
                     Theologis A., Ecker J. A., Paulo K., Bowman C.L., Brooks S.Y., An Theologis A., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., An Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M. K., Conway A.B., Conway A.B., Creasy T.H., Dewar K., Buehler E., Chan L., Conway A.B., Conway A.B., Creasy T.H., Dewar K., Chung M. K., Conl L., Conway A.B., Conway A.B., Crong B., Fujii C.Y., A. Gill J.E., Goldemith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., A. Kim C.J., Zohkins J., Johnson-Hopson C., Khan S., Khan A., Lam B., A. Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liucs J.S., Maiti R., Marziali A., Milischer J., Miranda M., Nuyen M., Nierman W.C., Osborne B.I., A. Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Soulhwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

""" "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB=Leaf;
Sugitatio B., Sakakibara H., Sugiyama T.;
Sugitatio B., Sakakibara H., Sugiyama T.;
Sugiterential Expression of Two Genes for Sucrose-Phosphate Synthase in Sugarcane: Molecular Cloning of the CDNAs and Comparative Analysis of Gene Expre sign.",
In Submitted (PRB-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AB001337; BAA19241.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 36; DB 10; Length 1047; 66.7%; Pred. No. 1.4e+02; ive 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 10; Length 460;
Pred. No. 56;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1047 AA; 116379 MW; DOEDB34961E1D83D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 AA; 50564 MW; E94B27B5C4B249EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1047 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AC012679; AAG52073.1; -. InterPro; IPR002471; Prol endopep ser. InterPro; IPR000379; Ser estrs site. PROSITE; PS00708; PRO ENDOPEP SER; I. Hypothetical protein.
MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharum officinarum (Sugarcane)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEWBLrel. 03, 01-MAY-1997 (TrEWBLrel. 03, 01-MAR-2003 (TrEWBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 EEDVPSAMDY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:| |||:|
414 VIPPGMDFS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4547;
```

SOSPS1.

P93782 P93782

RESULT 9

셤

ò

SEQUENCE

Query Match

ò 요

ö

Gaps

```
NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                               QBXPA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            052367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     052367
                                                                           Š
                                                                                                                   셤
                                                                                                                                                                                                                                                                     ACCOCCOS DESTANTA SERVINA SOUR SERVINA SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza Bativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Gill;
Webiranch D., Towle D.W.;
Wa+/H+-exchanger and Na+/K+/2Cl- -cotransporter are expressed in gills of the euryhaline Chinese crab Eriocheir sinensis.";
Comp. Biochem. Physiol. 126:S158-S158 (2000).
EMBL; AF301160; AAG39938.1; -.
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsunoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 36; DB 10; Length 1100; 66.7%; Pred. No. 1.5e+02; ive 2; Mismatches 1; Indels (
  Length 1084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eriocheir sinensis (Chinese mitten crab).

Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;

Bubrachyura; Grapsoidea; Varunidae; Eriocheir.
66.7%; Score 36; DB 10; Length 10
66.7%; Pred. No. 1.5e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001557; L_LDH.
InterPro; IPR001557; L_LDH.
Pfam; PP00534; Glycos transf_1; 1.
PROSITE; P00064; L_LDH; 1.
SEQUENCE 1100 AA; 121170 MW; 084F4604BA389CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003437; BAB86107.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 219
219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;
                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TYEMBLrel. 21, Created)
01-JUN-2002 (TYEMBLrel. 21, Last sequence update)
01-JUN-2003 (TYEMBLrel. 23, Last annotation update)
Putative sucrose-phosphate synthase.
P0678F11.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Na+/K+/2Cl-cotransporter (Fragment).
                                                                                                                                                                                                                                                                     PRT; 1100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                           |:| |||:|
453 VIPPGMDFS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 VIPPGMDFS 477
                                                                                               3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
6, Conserve
                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gramene; Q8S064; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone: P0678F11."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
NON TER
SEQUENCE
  Query Match
                                                                                                                                                                                                                                                                088064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09G004
                         Best Loc
Matches
                                                                                                                                                                                                                   RESULT 12
Q8S064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            096004
                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                            Gaрв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosenbluch M., Hynes M.F., Martinez-Romero B.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: ZINC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=13 / Type A;
PubMed=11792842;
Shidnizu T., Ohtani K., Hirakawa H., Ohehima K., Yamashita A.,
Shidni T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pRtrCFN299a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.8%; Score 35; DB 16; Length 253; 50.0%; Pred. No. 46; 2; Indels ive 3; Mismatches 2; Indels
     5; Length 219;
                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flesh-eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).

EMBL. AP10.1185; BAB79763.1;
InterPro; IPR000205; NAD.binding.
InterPro; IPR000594; ThiF_domain.
Pfam; PF00899; ThiF; I complete protecome.

Proc. Ap1. Sci. 27714 MM; 814DF79D3E0D7486 CRC64;
                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UJUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein CPE0057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aryl-alcohol dehydrogenase homolog (Fragment).
     Score 35; DB 5
Pred. No. 39;
1; Mismatches
                                                                                                                                                                                                           253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 AA.
   ов
39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF036920; AAC04779.1; -.
InterPro; IPR002328; ADH zinc.
InterPro; IPR002005; Adh zn family.
InterPro; IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
 64.8%;
75.0%;
Query Match
Best Local Similarity 75.0°
Matches 6; Conservative
                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||::| :||
108 BEIIPDDVDY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EBVVPXGMDY 10
                                                                                                   107 VPOGLDYS 114
                                                                          4 VPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CFN299;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium tropici
```

```
DR Pfam; PP00107; adh_zinc; 1.

DR PROSITE; P800059; ADH_ZINC; 1.

KW Metal-binding; Oxidoreductase; Zinc; Plasmid.

FT NON TER 298 A2; 31092 MW; 49BZF8117C33AB87 CRC64;

Query Match

G4.8%; Score 35; DB 2; Length 298;

Best Local Similarity 50.0%; Pred. No. 55;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EVVPXGMDYS 11

Cy 2 EVVPXGMDYS 11

Db 250 EIIPEGADFS 259

Search completed: December 22, 2003, 17:51:29

Job time: 25.2667 secs
```

virus virus virus virus virus

virus virus virus virus virus

virus virus virus virus virus virus

Hepatitis

virus virus virus

virus virus virus virus virus virus

Sequence:

Run on:

Searched:

Minimum Maximum Database

Result No.

```
/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "D-form residue"
ABB6052
ABB6025
ABB6025
ABB6054
ABB6055
ABB6055
ABB6055
ABB6055
ABB6055
ABB6055
ABB6056
ABB6056
ABB6056
ABB6053
                                                                                                                                                                                                                                                                                                                ABB80545
ABB80552
ABB80553
ABB80553
ABB80550
ABB80550
ABB80550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB80524 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
 11
/note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80524
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
ABB80524
 Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chance to have a result being printed,
                                                                       December 22, 2003, 16:41:00; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                      A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
| SIDSI/g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to hecore greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                         1107863
         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                 1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80528
ABB80529
ABB80561
ABB80562
ABB80542
ABB80542
ABB80543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB80524
                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H
                                                                                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                  US-09-909-164-13
54
                                                                                                                                          1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333333333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                    Copyright
                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        966.3
966.3
966.3
966.3
87.0
87.0
85.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   oţ
                                                                                                                                                                                                                                              seq
seq
                                                                                                                     Title:
Perfect score:
                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        522222444
522224444
64472444
                                                                                                                                                                                                                       Total number
                                                                                                                                                                                                                                            88
                                                     OM protein
```

```
11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus protease
                   virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lim-wilby M,
                                                                                                                                                                                                                                                                                  08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
                                                                                                                                                                                                                                                                                                                                               Synthetic
Novel pep
activity
                                                                                                                            Sequence
                                                                                                                                                                                                                                                               ABB80529;
                                                                                                                                                                                                                                                                                                                               virucide
                                                                                                                                                                                                                             RESULT 3
                                                                                                                                                                                                                                       ABB80529
                                                                                                                                                                                                                                                                ŝ
                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                       ô
                                                                                                                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoanide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                     DB 23; Length 11; 0.0018; hes 0; Indels
                                                                                                                                                                                                                     Query Match 96.3%; Score 52; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brunck TK;
                                                                                                                                                                                                                                                                                                                       ABB80528 standard; peptide; 11 AA.
                                     Brunck TK;
                                                                                                           Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2000; 2000US-220101P
21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                         1
                                                                                                                                                                                                                                                         1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORV-) CORVAS INT INC
                   (CORV-) CORVAS INT INC
                                     Levy OE,
                                                                                                                                                                                                                                                                         1 EBVVPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPI; 2002-361643/39
                                                      WPI; 2002-361643/39
                                                                                           virus protease -
                                                                                                                                                                                                    11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                     Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                          08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                         ABB80528;
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      virucide
                                                                                                                                                                                                                                                                                                     RESULT 2
                                                                                                                                                                                                                                                                                                               ABB8052
                                                                                                                                                                                                                                                                                                                                         셤
ð
```

```
/note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
peptide compound having hepatitis C virus protease inhibitory
lty useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.3%; Score 52; DB 23;
100.0%; Pred. No. 0.0018;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŢĶ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80529 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 64; 69pp; English.
                                                                                                                              Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-361643/39.
```

is useful for treating disorders associated with hepatitis C virus.

```
ö
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat alsorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41
                                                                                                                                                                            ö
                                                                                                                                                Length 11;
                                                                                                                                                                         0; Indels
                                                                                                                                           96.3%; Score 52; DB 23;
100.0%; Pred. No. 0.0018;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                         Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Norvalyl
                                                                                                                                                                                                                                                                                                        ABB80561 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                           Conservative
                                                                                                                                                                                                      11
                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levy OB,
                                                                                                                                                                                                      EEVVPXGMDYS
                                                                                                                                                                                                                                 EEVVPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-361643/39.
                                                                                                                                                          Similarity
                                                                                                                  11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                               08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                                                                      11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                    ABB80561;
                                                                                                                                                                                                                                                                                                                                                                                                                                         virucide.
                                                                                                                                             Query Match
                                                                                                                                                            Local
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                            ABB8056
                                                                                                                                                                                                                                                                             RESULT
셤
                                                                                                                                                                                                                                                                                                                    ò
```

```
'note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Bequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                           Gaps
                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42
                                                                           .
                                                  Length 11;
                                                                          Indels
                                      DB 23; Le... 0.0018;
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                 Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                        ABB80562 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck TK;
                                       96.3%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-220101P.
                                                                                                                                                                                                                                          (first entry)
                                               Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                  1 EEVVPXGMDYS 11
                                                                                                                          1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-361643/39.
                         11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus protease
                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-2000;
                                                                                                                                                                                                                                          08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2002
                                                                                                                                                                                                                                                                                                                                  Synthetic.
                         Sequence
                                                                                                                                                                                                                  ABB80562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                         virucide
                                                                                                                                                               RESULT 5
                                                                                                                                                                             ABB80562
                                                                                                                                                                                                                 SXCCCCCCX8XTFIXERXBXBXBXBXBXBXBIIIIIIIIIIIIII
SXS
                                                                                                                        셤
                                                                                                   ઠે
```

ઠે 셤

```
"Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
                                                                                                                                                                                                                                                                             'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                      /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                         'notes "D-form residue"
                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AA.
                                            ABB80542 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.0%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80543 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000; 2000US-220101P.
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BEVVPXGQDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AA;
                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus protease
                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                         08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2002
                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gарв
                                Gaps
                                                                                                                                                                                                                                                                                             Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 23; Length 11;
Pred. No. 0.017;
0; Mismatches 1; Indels
DB 23; Length 11;
0.0018;
hes 0; Indels
th 96.3%; Score 52; DB Similarity 100.0%; Pred. No. 0.0 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunck TK;
                                                                                                                                                                      ABB80538 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2001, 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.98;
                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 90.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEVVPXGQDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 REVVPXGMDYS 11
                                                                                         11
                                                             1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
                                                                                 EEVVPXGMDYS
                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                  08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2002
                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                   ABB80538;
                                                                                                                                                                                                                                                                                                            virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
 Query Match
                                                                                                                                      RESULT 6
                                                                                                                                                      ABB80538
```

```
ö
The sequence represents a peptide compound of the invention having the peptides of the inveptides of view (HVV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 23;
Pred. No. 0.017;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-2002
```

셤 ઠ

```
"Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                        peptide compound having hepatitis C virus protease inhibitory
Ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 23; Length 11; Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                              'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carbonyl
                                                                                                                                           "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 9 /note= "D-form residue"
                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80522 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Norvalyl residue 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 64; 69pp; English
                                                                                                               residue
                                                                                                                                                                                                                                                                                                                                         Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.2%;
90.9%;
                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                        19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10, Conservative
                                                                                                                              11
/note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 BEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EBVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                              /note=
                                                                                                                                                                                                                                                                                                         (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                        Levy OE,
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                           WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                         virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                             Modified-site
                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                         Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-2002
                                                                                                                                                                                                           31-JAN-2002
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virucide
                                                                                                                                                                                                                                                                                                                                                                                                         Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
ZXEXEXEXEXEXE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                         "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ingredient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   armaceutical composition comprising the peptide as an active inguseful for treating disorders associated with hepatitis C virus
             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 23; Length 11; Pred. No. 0.017; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                         "C-terminal amide"
                                                                                                                                                                                                                                        note= "D-form residue"
                                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80521 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEVVPXGQDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEVVPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AA;
                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                      WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus protease
                                                                                                                              Key
Modified-site
                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002
                                                                                            Synthetic.
                                                              virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nove1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

RESULT

셤

ઠે

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide;
                                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 23;
Pred. No. 0.026;
); Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brunck TK;
                                                                                ŢĶ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80526 standard; peptide; 11 AA.
                                                                                                                                                                                                                  Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                       85.2%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2001; 2001WO-US23169.
              21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 BEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lim-wilby M, Levy OE,
                                               (CORV-) CORVAS INT INC
                                                                                Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    æ
                                                                                                                                                                                                                                                                                                                                                                                        11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                     virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virucide
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                    hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
11
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                    Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80525 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.2%;
                                                                                                                19-JUL-2001; 2001WO-US23169
                                                                                                                                                 21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEVVPXGMSYS 11
                                                                                                                                                                                                                    Levy OE,
                                                                                                                                                                                 (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                  API; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AA;
                                                                                                                                                                                                                                                                                                                       virus protease
                                               WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208251-A2
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                  Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2002.
                                                                                31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB80525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
```

g ઠે

ö

Gaps

Length 11;

Score 46; DB 23; Pred. No. 0.026; 0; Mismatches

85.2%;

```
hepatitis C virus (MCV) protease inhibitory activity. The peptides of the
                                                          pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                          Best Local Similarity 50.5
Matches 10; Conservative
                                                                                                   11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                           08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                              ABB80548;
                                                                                                                                                                                                                                                                                                                                                                                                                  virucide.
                                                                                                                             Query Match
  8888888888
                                                                                                                                                                                                            셤
                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                ö
                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Norvalyl carbonyl forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                Gaps
                                 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C tease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                  Score 46; DB 23; Length 11;
Pred. No. 0.026;
0; .Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck TK;
                                                                                                Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80547 standard; peptide; 11
                                                                                                                                                                                                                                                                85.2%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                     EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-361643/39.
              WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levy
                                                                                                                                                                                                                                       11 AA;
                                                                      virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200208251-A2
                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Modified-Bite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-2002
                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB80547;
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virucide.
                                          Novel
                                                                                                                                                                                                                                                                                               Matches
요
```

ઠે

The sequence represents a peptide compound of the invention having

Claim 17; Page 65; 69pp; English

```
ö
                                                                                                                                                                                                                                                                                                                                           /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
  Gapa
                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.
  ö
1; Indels
                                                                                                                                                                                                                                                                                                                   'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                           "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 65; 69pp; English.
                                                                                                                ABB80548 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-2000; 2000US-220101P.
                                                                                                                                                                     (first entry)
                                            1 EEVVPXGTDYS 11
                         11
                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORV-) CORVAS INT INC
                        1 REVVPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AA;
                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                              /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                             Gaps
                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
Score 46; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                     note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                      11
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                    note= "D-form residue"
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                ABB80551 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.2%;
Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                    1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                    08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                            ABB80551;
                                                                                                                                                                                                                                                                        virucide.
                                                                                                                       RESULT 15
                                                                                                                                     ABB8055
                                                                                                                                                                            a
                                                        ઠે
```

දු ද

```
Search completed: December 22, 2003, 17:41:01 Job time : 32.4667 secs
```

us-09-909-164-13.rai

```
Conservative
                                   TYPE: PRT
ORGANISM: Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Citrus unshiu
US-08-853-9488-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 VIPPGMDFS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 WPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            US-08-853-948B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-853-948B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Applisequence 11, Applisequence 11, Applisequence 12, Applisequence 12, Applisequence 14, Applisequence 8, Applisequence 6, Applisequence 2, Applisequence 4, Applisequence 2, Applisequence 4, Applisequence 6, Applis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Appli
Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                               December 22, 2003, 16:37:03 ; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Ag
Sequence 24, A
Sequence 10, A
Sequence 11, A
Sequence 7, Ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4
Sequence 4
Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-853-948B-4
US-09-873-948B-5
US-09-873-87-24
US-09-134-272-10
US-09-134-272-10
US-09-134-272-4
US-09-03-134-272-4
US-09-334-272-4
US-09-394-272-4
US-09-885-114-82
US-09-885-114-82
US-09-885-418-8
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  protein search, using sw model
                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                 US-09-909-164-13
54
1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1068
1068
1068
1068
1081
1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
378
378
473
765
801
811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
102
152
152
152
                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .......
                                                                                                                                                                                 Perfect acore:
                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein
                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
No.
```

```
4172, Ap
6, Appli
6, Appli
4, Appli
4, Appli
6, Appli
23, Appli
                                                                                                                                                        Sequence 4,
Sequence 4,
                                                                                                            Sequence
Sequence
Sequence
Sequence
                                             Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                             Sequence
                                                                                                                                                                                        Sequence
                         Sequence
                                   Sequence
US-08-193-977-7
US-08-464-517-21
US-08-463-517-21
US-08-463-772-21
US-08-926-8428-20
US-08-926-8428-20
US-08-926-8428-22
US-08-926-8428-21
US-08-926-8428-21
US-08-926-8428-21
US-08-926-8428-21
US-08-926-8428-21
US-08-463-772-6
```

ALIGNMENTS

```
Sequence 4, Application US/08853948B
Sequence 4, Application US/08853948B
Sequence 4, Application US/08853948B
Serent No. 6210943
GENERAL INFORMATION:
APPLICANT: AKIHAMA, Toyota
TITLE OP INVENTION: SUCROSE PHOSPHATE SYNTHASE PROM CITRUS AND DNA ENCODING
TITLE OP INVENTION: THE SAME
TITLE OP INVENTION: THE SAME
TITLE OP INVENTION: THE SAME
CURRENT APPLICATION NUMBER: US/08/853,948B
CURRENT PILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 4
LENGTHER: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5. Application US/08853948B
Patent No. 6210943
GENERAL INPORMATION:
FULLE INPORMATION:
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING TITLE OF INVENTION: THE SAME FILE REPERENCE: 0049-0235-0 CURRENT APPLICATION NUMBER: US/08/853,948B
CURRENT PILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERTURE:

OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg,
OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys,
OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 36; DB 3; Length 341; 66.7%; Pred. No. 18; ive 2; Mismatches 1; Indels
```

ઠે 셤

```
Sequence 11, Application US/08429054A
Patent No. 5917126
GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: UZAN; VOELKER, TONI; GERVALS, MONICA
TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 36; DB 2; Length 1068; 66.7%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Van Assche, C.
APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Voelker, T.
TITLE OF INVENTION: MODIFICATION OF SUCROSE
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: LOAD

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: INP PC COMPATIBLE
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,054A
FILING DATE: 26-APR-1995
CTASSIFICATION BAR:
APPLICATION NUMBER: US 842,337
FILING DATE: 20-March-1992
APPLICATION NUMBER: US 842,337
FILING DATE: 18-July-1991
CTASSIFICATION NUMBER: PCT/FR 91/00593
FILING DATE: 20-July-1991
CTASSIFICATION NUMBER: French 90402094.9
FILING DATE: 20-July-1990
CTASSIFICATION NUMBER: 18-July-1990
CTASSIFICATION NUMBER: 18-July-1990
CTASSIFICATION NUMBER: 18-July-1990
CTASSIFICATION NUMBER: 146.1137
FILING DATE: 10-July-1990
CTASSIFICATION NUMBER: 146.1137
FELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 146.1137
FELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 661-8000
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: BIERNAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08718777
Patent No. 5981852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TENGTH: 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 WPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: Amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-429-054A-11
       US-08-429-054A-11
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-718-777-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-394-272-10
Sequence 10, Application US/09394272
Sequence 10, Application US/09394272
Sequence 10, Application US/09394272
Sequence 10, Application General Information:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 36; DB 4; Length 1049; 66.7%; Pred. No. 67; 1; Indel8
       Score 36; DB 3; Length 348;
Pred. No. 19;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.7%; Score 36; DB 4; Length 368; Best Local Similarity 66.7%; Pred. No. 20; Matches 1; Indels Matches 1; Indels
                                                                                                                                                                                                                                                Sequence 24, Application US/09697367

| Sequence 24, Application US/09697367
| Patent No. 6323015
| GENERAL INFORMATION:
| APPLICANT: Orozco Jr., Emil M.
| APPLICANT: Orozco Jr., Emil M.
| APPLICANT: Meng, Zude
| APPLICANT: Tarczynski, Mitchell
| TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
| FILE REFRENCE: BB1166 US NA.
| CURRENT APPLICATION NUMBER: US/09/697,367
| CURRENT FILING DATE: 1998-MAY-07
| PRIOR PPLICATION NUMBER: PCT/US99/09865
| PRIOR PRILING DATE: 1999-MAY-06
| NUMBER OF SEQ ID NOS: 24
| SOFTWARE: Microsoft Office 97
            66.7%;
66.7%;
Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.7
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:| |||:|
217 VIPPGMDFS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 VIPPGMDFS 444
                                                                                                                                       |:| |||:|
234 VIPPGMDFS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMDYS 11
                                                                                                         3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Zea mays
US-09-697-367-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 10
LENGTH: 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-394-272-10
                                                                                                                                                                                                                                                US-09-697-367-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 24
LENGTH: 368
```

Š g ઠે g

```
US-09-394-272-8

Sequence 8, Application US/09394272

Sequence 8, Application US/09394272

Sequence 8, Application US/09394272

Sequence 8, Application US/09394272

GENERAL INFORMATION:

APPLICANT: Holdedy, A. Scott

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE PATENTIN Ver. 2.0

SEQ ID NO 8

LENGTH: 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09394272
| Patent No. 647288
| GENERAL INFORMATION:
| APPLICANT: Holaday, A. Scott | TILLE OF INVENTION: TRANSCENIC FIBER PRODUCING PLANTS WITH INCREASED | TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE | PILE REFERENCE: 201304/1000 | CURRENT PILLING DATE: 1999-09-10 | CURRENT FILLING DATE: 1999-09-10 | NUMBER OF SEQ ID NOS: 14 | SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 36; DB 3; Length 1068; 66.7%; Pred. No. 68; 1; Pred. 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 36; DB 4; Length 1068; 66.7%; Pred. No. 68; 1; Indels tive 2; Mismatches 1; Indels
             FILING DATE: 25-OCT-1996

APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-OCT-1995

PRIOR APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-OM-1995

APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-OM-1995

ATTORNEY/AGENT INFORMATION:
NAME: BAIDARA RAG-Venter. Ph.D., REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: 32,750

TELEPHONE: (415)328-4400

TELEPHONE: (415)328-4477

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-051-341-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Zea mays
US-09-394-272-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-394-272-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09051341

Patent No. 6124528

GENERAL INFORMATION:

APPLICANT: Shewmaker, C. K.

TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440

CITY: Palo Alto
CITY: Palo Alto
CITY: Palo Alto
COUNTRY: USA
ZIP: 94306
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN DATA:
APPLICATION NUMBER: US/09/051,341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 36; DB 2; Length 1068;
66.7%; Pred. No. 68; 1; Indels
tive 2; Mismatches 1; Indels
TITLE OF INVENTION: PHOSPHATE

TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE LAW Offices of Barbara Rae-Venter
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
CUNTRY: USA
ZIP: 94306
COMPUTER: ISA
COMPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1068 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-777-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-051-341-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      È
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
STATE: PA
COUNTRY:
                  US-08-569-147-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                              GENERAL INCORNATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 36; DB 4; Length 1084;
66.7%; Pred. No. 69;
tive 2; Mismatches 1; Indels
                                                                                                                DB 4; Length 1081;
69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.7%; Score 36; DB 4; Length 1083; Best Local Similarity 66.7%; Pred. No. 69; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                       1; Indels
                                                                                                                                                     2; Mismatches
                                                                                                                  Score 36;
Pred. No.
                                    TYPE: PRT
ORGANISM: Craterostigma plantagineum
                                                                                                                                                                                                                                                                                                        US-09-394-272-11
; Sequence 11, Application US/09394272
; Patent No. 6472588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-394-272-9
; Sequence 9, Application US/09394272
; Patent No. 6472588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-394-272-11
                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                     |:| |||:|
445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 VIPPGMDFS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDYS 11
                                                                                                                                                                                             3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 11
LENGTH: 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 9
LENGTH: 1084
SEQ ID NO 4
LENGTH: 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-394-272-9
                                                                          US-09-394-272-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                             ઠે
```

```
195-08-551-47.

196-08-551-47.

196-08-551-47.

196-08-551-47.

196-08-551-47.

197-08-08-197-197.

197-08-08-197-197.

197-08-08-197-197.

197-08-08-197-197.

197-08-08-197-197.

197-08-08-197-197.

197-08-08-197-197.

197-08-197-197-197.

197-08-197-197-197.

197-08-197-197-197.

197-08-197-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-197-197.

197-08-1
```

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31637, Application US/09252991A
Sequence 31637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31637
LENGTH: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.0%; Score 34; DB 4; Length 1065; Best Local Similarity 85.7%; Pred. No. 1.7e+02; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.0%; Score 34; DB 3; Length 140; Best Local Similarity 75.0%; Pred. No. 16; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-963-851-14

Sequence 14, Application US/08963851

Patent No. 6300116

GENERAL INFORMATION:

APPLICANT: VAN DER OSTEN, CLAUS

APPLICANT: HALKIER, TONDEN

APPLICANT: BAUDITZ, PETER

APPLICANT: BAUDITZ, PETER

APPLICANT: HANSEN, PETER KAMP

TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS

FILE REFERENCE: 4946,200-US

CURRENT APPLICATION NUMBER: US/08/963,851

CURRENT APPLICATION NUMBER: 1997-11-04

NUMBER OF SEQ ID NOS: 35

SOFTAMER PARISED FOR WINDOWS VERSION 3.0
CLASSIFICATION: 536

ATORNEY/AGENT INFORMATION:
NAME: TRUJILIO, DOTEON TRUJILO, DOTEON TRUJILO, DOTEON TRUJILO, DOTEON TRUJILO, DOTEON TRUJILO, DOTEON TRUJILO, TRUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1065
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 WPTGFDY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 PQGMDYS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-252-991A-31637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-31637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
```

```
Query Match 66.7%; Score 36; DB 12; Length 126; Best Local Similarity 66.7%; Pred. No. 14; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 WPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:| |||:|
23 VIPPGMDFS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-10-289-757-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 946, App
Sequence 168, App
Sequence 10, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 11, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 4, Appli
Sequence 4, Appli
                                                                                                                                                                          December 22, 2003, 16:40:14 ; Search time 20.8667 Seconds (without alignments) 98.451 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCCMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
3: /cgn2_6/ptodata/2/pubpaa/BCT_MBW_PUB_pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NBW_PUB_pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NBW_PUB_pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB_pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCCMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCCMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCCMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCCMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCCMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCCMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCCMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCCMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCCMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCCMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 US-10-393-840-946
2 US-10-289-757-73
5 US-10-289-757-16
5 US-10-289-757-10
5 US-10-289-757-71
5 US-10-217-700-8
6 US-10-217-700-8
7 US-10-217-700-9
10S-09-813-408-27
1 US-09-813-408-27
1 US-09-813-408-27
2 US-10-029-815-42-5111
2 US-10-029-815-442-5111
2 US-10-029-815-442-5111
2 US-10-029-815-442-5111
2 US-10-029-815-442-5111
2 US-10-029-815-442-5111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         696363 seqs, 186758610 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                     US-09-909-164-13
54
1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
937
938
1069
1068
1088
1084
588
222
1062
247
240
3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       666.77
666.77
666.77
666.77
666.77
666.77
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
666.78
66
                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
```

```
Sequence 14, Appliance 14, Appliance 12116, A Sequence 12697, A Sequence 12118, A Sequence 126, Appliance 526, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 946, Application US/10393840

Publication No. US20030229922A1

GENERAL INFORMATION:

APPLICANT: Blokaberg, Leonard N.

ITILE OF INVENTION: Materials and Methods for the

FILE REFERENCE: 11000.1012c3

CURRENT APPLICATION: WOMBER: US/10/393,840

FRIOR PILING DATE: 2000-08-10

FRIOR PILING DATE: 1998-10-13

PRIOR PILING DATE: 1998-10-13

FRIOR PILING DATE: 1998-10-13

FRIOR PILING DATE: 1999-10-13

FRIOR PILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 956

SOFTWARE: PREASEQ for Windows Version 4.0

SEQ ID NO 946

LENGTH: 126
                       Sequence Sequence 1
US-10-034-623-4

US-10-027-801-4

US-09-986-930-16

US-09-978-626-4881

US-09-978-626-4881

US-09-978-626-4881

US-09-978-626-4881

US-09-978-626-626

US-09-978-198-526

US-09-978-198-526

US-09-978-198-526

US-09-978-198-526

US-09-978-526-108-526

US-09-978-526-108-526

US-09-978-526-108-526

US-09-978-526-108-526

US-09-978-526-108-526

US-09-978-526-108-526

US-09-978-824-526

US-09-978-824-526

US-09-978-824-526

US-09-978-824-526

US-09-978-824-526

US-09-978-824-526

US-09-978-824-526

US-09-978-830A-526

US-09-978-830A-526

US-09-978-830A-526

US-09-978-830A-526

US-09-978-830A-526

US-09-978-830A-526

US-09-978-830A-526

US-09-978-830A-526

US-09-978-830A-526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-978-375A-526
US-09-978-188A-526
US-09-978-298A-526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
    ; ORGANISM: Pinus radiata
US-10-393-840-946
```

Gaps

```
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSCENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: TRANSCENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT PILING DATE: 1999-09-10
FARLIER FILING DATE: 1999-09-10
FARLIER FILING DATE: 1999-09-10
FARLIER FILING DATE: 1099-09-10
FARLIER FILING DATE: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 12; Length 1062;
Pred. No. 1.5e+02;
2; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 15; Length 1049;
Pred. No. 1.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Denmer, Jeroen
APPLICANT: Porster, Richard L
APPLICANT: Forster, Richard L
APPLICANT: Gibson, John Bryan
APPLICANT: Gibson, John Bryan
APPLICANT: Gibson, Michael Andrew
APPLICANT: No. US20030180751Alriss, Geoffrey
APPLICANT: No. US2003180751Alriss, Geoffrey
APPLICANT: All Matthew
APPLICANT: All Sallsbury, Keith Martin
APPLICANT: Hall, Claire
TITLE OF INVENTION: Compositions isolated from forsge
TITLE OF INVENTION: Compositions isolated from forsge
FILE REFERENCE: 11000.1661U
CURRENT PAPLICATION NUMBER: US/10/289,757
CURRENT FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ. ID NOS: 218
SOSTWARRE FREUSCE for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 71, Application US/10289757 Publication No. US20030180751A1 GENERAL INFORMATION:
US-10-217-700-10
; Sequence 10. Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Festuca arundinacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haigler, Candace H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          466 VIPPGMDFS 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-289-757-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-289-757-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-217-700-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 12; Length 938;
Pred. No. 1.3e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 36; DB 12; Length 937; 66.7%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INCORPATION:

APPLICANT: Demoner, Jercen
APPLICANT: Forster, Richard L
APPLICANT: Glabon, John Bryan
APPLICANT: Glabon, Michael Andrew
APPLICANT: Shemk, Michael Andrew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Composition isolated from forage
TITLE OF INVENTION: 11000.1061U
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/337,703
PRIOR APPLICATION NUMBER: 60/337,703
PRIOR SEQ ID NOS: 218
SEQ ID NO 168
ELENCTH: 338

***MINISTREMENT OF THE OFFICE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                      APPLICANT: Counter, Richard L
APPLICANT: Counter, Richard L
APPLICANT: Glbson, John Bryan
APPLICANT: Shenk, Michael Andrew
APPLICANT: Shenk, Michael Andrew
APPLICANT: Glbson, John Bryan
APPLICANT: Glbson, Matthew
APPLICANT: Hall, Claire
TITLE OF INVENTION: Compositions isolated from forage
FITLE OF INVENTION: grasses and methods for their use
FILE REPERBURE: 11000, 1061U
CURRENT APPLICATION NUMBER: US/10/289,757
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/337,703
PRIOR APPLICATION NUMBER: 60/337,703
FRIOR PILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 168, Application US/10289757
Publication No. US20030180751A1
         Sequence 73, Application US/10289757
Publication No. US20030180751A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.7
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Lolium perenne
US-10-289-757-168
                                                                                                                                               APPLICANT: Demmer, Jeroen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Lolium perenne
US-10-289-757-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| |||:|
462 VIPPGMDFS 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 VIPPGMDFS 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-289-757-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
```

ò g

ö

Gapa

ö

ö

Gaps

ö

RESULT 4

g

ઠે

```
LENGTH: 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-813-408-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-217-700-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 27
                                                                                                                                                                                                              ⋩
                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      음
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-217-700-11

Sequence 11, Application US/10217700

Publication No. US20030070191A1

GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT PELLON NUMBER: US/10/217,700
CURRENT FILING DATE: 1999-09-10
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER FILING DATE: 1999-09-10
SOFTWARE: PATENTING DATE: 1999-09-10
SOFTWARE: PATENTING US: 14
SSOFTWARE: PATENTING US: 14
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201344/1000
CURRENT APPLICATION NUMBER: US/10/217,700
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.0
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 36; DB 15; Length 1068; 66.7%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.7%; Score 36; DB 15; Length 1081; Best Local Similarity 66.7%; Pred. No. 1.6e+02; Matches 6; Conservative 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Craterostigma plantagineum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 4, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| |||:|
435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Zea mays
US-10-217-700-8
                                                                                                                                                                                                                                                        1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 4
LENGTH: 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-217-700-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-217-700-4
                                                                                                                                                                                                                              SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
Sequence 27, Application US/09813408
Publication No. US20030049619A1
GENERAL INFORMATION:
APPLICANT: Delagrave, Simon
APPLICANT: Marrs, Barry
TITLE OF INVENTION: Methods For The Synthesis Of Polynucleotides And Combinatorial
TITLE OF INVENTION: OF Polynucleotides
FILE REFERENCE: HERO41
CURRENT APPLICATION NUMBER: US/09/813,408
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 85
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/10217700

| Sequence 9, Application US/20030070191A1
| Publication No. US20030070191A1
| Publication No. US20030070191A1
| GENERAL INFORMATION:
| APPLICANT: Holaday, A. Scott
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| TITLE OF INVENTION NUMBER: 09/394,272
| EARLIER APPLICATION NUMBER: 09/394,272
| EARLIER APPLICATION NUMBER: 09/394,272
| RARLIER PAPELICATION NUMBER: 09/394,272
| SARLIER PAPELICATION OF: 2.0
| SOFTWARE PATENTING DATE: 1999-09-10
| SOFTWARE PATENTING DATE: 1999-09-10
| SOFTWARE PATENTING DATE: 1990-09-10
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 15; Length 1084; Pred. No. 1.6e+02; 2; Mismatches 1; Indels (
                                                                                                               Length 1083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 11; Length 440;
Pred. No. 92;
2; Mismatches 1; Indels
                                                                                                            Query Match 66.7%; Score 36; DB 15; Best Local Similarity 66.7%; Pred. No. 1.6e+02; Matches 6; Conservative 2; Mismatches 1.
; LENGTH: 1083
T TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-217-700-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.70,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 440

; TYPB: PRT

; ORGANISM: Aeropyrum pernix

US-09-813-408-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 VIPPGMDFS 461
                                                                                                                                                                                                                                  |:| |||:|
483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 EVLPWGVDY 128
                                                                                                                                                                                                      3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGMDY 10
```

```
Sequence 4, Application US/10029120

Sequence 4, Application US/10029120

Publication No. US20030175708A1

GENERAL INFORMATION:
APPLICANT: Swanson, Rohat A.
APPLICANT: Selleper, Christa

TITLE OF INVENTION: UUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A

CURRENT APPLICATION NUMBER: US/10/029,120

CURRENT PILING DATE: EARLIER FILING DATE: 1999-09-29

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FASELSEQ for Mindows Version 3.0

SEQ ID NO 4
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1062;
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OP INVENTION: Prokaryotes
FILE REPREMENCE: ELLINA JOHA PLICALION UNDERF: US/09/815,242
CURRENT PILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
   Indels
..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.0%; Score 34; DB 9; I
85.7%; Pred. No. 3.9e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILLING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
   Mismatches
                                                                                                                                                                                                                                                              Sequence 5111, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
3,
                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7
Matches 6; Conservative
5, Conservative
                                                                                              201 KKIVPIGPDY 210
                                                        1 REVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 PQGMDYS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 PXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-815-242-5117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
Matches
                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ሯ
                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.9%; Score 34.5; DB 12; Length 588; 80.0%; Pred. No. 1.6e+02; ive 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 12; Length 222; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wells, Jeremy M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: INJURY, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: SOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
ITILE REFERENCE: 064335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT PILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PAECENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-091-007-58

Sequence 58, Application US/10091007

Sequence 58, Application US/10091007

PUBLICATION NO. US20030170782A1

GENERAL INFORMATION:

APPLICANT: Microbial Technics limited

APPLICANT: Henniffy, Sean B

TITLE REPERENCE: PWC/P21978W0

CURRENT APPLICATION NUMBER: US/10/091,007

CURRENT APPLICATION NUMBER: US/10/091,007

CURRENT FILING DATE: 1999-09-07

NUMBER OF SEQ ID NOS: 276

SEQ ID NO 58

LENGTH: 222
                                                                                    Sequence 1660, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-58
                                                                                                                                                                         APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 EEVVP-GMDF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-094-749-1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SULTRACTION 1660
```

ઠે 셤

```
NESOUR 12.

NESOUR 12.

NESOUR 12.

NESOUR 12.

Sequence 4, Application US/10027806

Sequence 4, Application US/10027806

Sequence 4, Application US/10027806

Sequence 4, Application WS/10020160476A1

Sequence 4, Application WS 0.

APPLICANT: Swanson, Robert A.

APPLICANT: Schlaper, Christer A.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM

TITLE OF INVENTION: NUMBER: US/10/027, 806

CURRENT FILING DATE: EARLIER PILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1999-09-29

PRIOR PILING DATE: EARLIER FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FREEEQ for Windows Version 3.0

LENGTH: 3472

TYPE: PRT

CORGANISM: Cenarchaeum symbiosum

US-10-027-806-4
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                    Gaps
                                                                                                                                                                                    ö
                                                                                                                            Query Match 63.0%; Score 34; DB 12; Length 3472; Best Local Similarity 45.5%; Pred. No. 1.5e+03; Matches 5; Conservative 4; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.0%; Score 34; DB 14; Length 3472; Best Local Similarity 45.5%; Pred. No. 1.5e+03; Matches 5; Conservative 4; Mismatches 2; Indels C
; LENGTH: 3472
; TYPE: PRY
CRGANISM: Cenarchaeum symbiosum
US-10-029-120-4
                                                                                                                                                                                                                                                              |:|:| |: |
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:| |: |
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                 1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

Search completed: December 22, 2003, 17:32:43 Job time : 20.9333 Becs

Н

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

December 22, 2003, 17:24:36; Search time 9.06667 Seconds (without alignments) 116.675 Million cell updates/sec Run on:

Title: Perfect score:

US-09-909-164-13 54 1 BEVVPXGMDYS 11 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | Description | hypothetical prote | conserved hypothet | V1 protein - tobac | sucrose-phosphate | sucrose-phosphate | unknown protein F2 | sucrose-phosphate | sucrose-phosphate | sucrose-phosphate | sucrose-phosphate | sucrose-phosphate | hypothetical prote | peptidoglycan-bind | probable alkaline | hypothetical prote | probable membrane | fat facets (faf) s | plastocyanin b - L | plastocyanin precu | plastocyanin b pre | 6-0-methylguanine- | O6-methylguanine-D | hypothetical prote | probable hexosyltr | L-lactate dehydrog | ABC transporter AT | phenylalanine-tRNA | succinate dehydrog |
|-----------|--------|--------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | | a | S54619 | D69551 | A42452 | S72649 | 872650 | G96764 | JC4783 | JQ1329 | T09837 | T04062 | T04103 | T24111 | H87660 | H72784 | T20173 | F69009 | B49132 | 800210 | 838255 | 858208 | AG3104 | D98182 | F72745 | G69290 | G69350 | E86665 | A70164 | F81138 |
| | • | DB | ~ | N | N | N | ~ | N | ~ | - | N | N | ~ | ~ | ~ | 7 | ~ | ~ | N | ď | ~ | ~ | N | N | N | 7 | ~ | ~ | N | 7 |
| | | Match Length | 156 | 363 | 102 | 341 | 348 | 460 | 1049 | 1068 | 1081 | 1083 | 1084 | 425 | 433 | 440 | 1150 | 1474 | 2747 | 66 | 155 | 168 | 290 | 290 | 296 | 357 | 366 | 265 | 266 | 587 |
| | Query | Match | 74.1 | 70.4 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 |
| | | Score | 40 | 38 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 35 | 35 | 35 | 35 | 35 | 32 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 |
| | Result | No. | - | 7 | 3 | 4 | S | 9 | 7 | 80 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | | 21 | 22 | | 24 | | 26 | 27 | 28 |

| disease resistance RND multidrug effi hypothetical prote hypothetical 167K partial transposas hypothetical prote fibroblast growth hypothetical prote hypothetical prote conserved hypothetical prote conserved hypothetical conserved hypothetical prote hypothetical prote in transposase ISCIO5 transposase ISCIO5 hypothetical prote hypothetical protein [1] | pantoate-beta-alan transposase ISC105 |
|---|--|
| 148899 F83335 T330830 A39427 A39471 A39471 B90335 SS7810 A96001 A96546 F90298 C50307 | G83055 B90487 |
| 0000000000000000000000000000000000000 | 0.00 |
| 908 1062 1062 3472 3472 1128 1128 225 247 257 262 262 | 283 |
| 633.0 633.0 633.0 611.1 611.1 611.1 611.1 | 61.1 |
| 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 333 |
| | 4 4 4 0 |

ALIGNMENTS

| - | |
|----|---|
| Ħ | ð |
| - | ~ |
| 0 | 9 |
| S | 4 |
| 24 | S |
| | |

| hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae) |
|--|
| Naticinara names: hypotherical protein ozeiz; hypotherical protein robsus.s C;Species: Saccharomyces cerevisiae |
| C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002 C;Accession: 854619: 866879 |
| Ride Haan, M.; Maarse, A.C.; Grivell, L.A. |
| submitted to the EMBL Data Library, May 1995 |
| A; Reference number: S54617 |
| A;Accession: S54619 |
| A; Molecule type: DNA |
| A;Residues: 1-156 <deh></deh> |
| A;Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:q829123 |
| Ride Haan, M.; Grivell, L.A.; Maarse, A.C. |
| |

submitted to the Protein Sequence Database, July 1996
A;Reference number: 866877
A;Reference number: 866877
A;Accession: 866879
A;Accession: 866879
A;Residues: 1-156
A;Residues: 1-156
A;Cross-references: EMEL: 274920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR
A;Experimental source: strain 5288C
C;Genetics:
A;Cross-references: SGD:S0005539
A;Map position: 15R
C;Superfamily: hypothetical protein YOR013**

Gaps ö 'Match 74.1%; Score 40; DB 2; Length 156; Local Similarity 77.8%; Pred. No. 1; 100servative 1; Mismatches 1; Indels Query Match Best Local & Matches

ö

2 EVVPXGMDY 10 50 EVMPLGMDY 58 Š 요

Conserved hypothetical protein AF2411 - Archaeoglobus fulgidus
Cispecies: Archaeoglobus
Cispecies:

disease resistance

2 T48898

906

63.0

34

29

g ઠે

```
unknown protein F25P22.17 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: G96764
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alons: Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K ansnen, N.F.; Hudghes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial.
Rizzo, M.; Rooney, T.; Rowartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon A; Authors: Salzberg, S.L.; Schwartz, J.C.; Davis, R.W.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A66141; MUID:21016719; PMID:11130712
A; Accession: G96764
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-460 <STO>
A; Residues: Leferences: GB:AE005173; NID:g6692750; PIDN:AAF24856.1; GSPDB:GN00141
             sucrose-phosphate synthase (BC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
C;Species: Citrus unshiu
C;Species: C14-0ct-1998 #sequence_revision 24-0ct-1998 #text_change 21-Jul-2000
C;Accession: S72650
R;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of CDNAs encoding three sucrose phosphate synt:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructo: A; Pathway: sucrose biosynthesis
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Status: 1-348 «XON»
A;Residues: 1-348 «XON»
A;Cross: references: EMBL:AB0006660; NID:92351059; PIDN:BAA22071.1; PID:92351060
A;Rxperimental source: fruit, cv. Miyagawa-Wase
A;Rxperimental source: fruit, cv. Miyagawa-Wase
A;Rxperimentel source: struit, cv. Miyagawa-Wase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2; Length 460;
Pred. No. 23;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 36; DB 2; Length 348; 66.7%; Pred. No. 17; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bucrose-phosphate synthase (EC 2.4.1.14) - rice C;Species: Oryza sativa (rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 66.7
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 EEDVPSAMDY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EBVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:| |||:|
234 VIPPGMDFS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S72650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Genetics:
A, Gene: F25P22.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JC4783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rimorris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992

A;Title: The nuclectide sequence of the infectious cloned DNA component of tobacco yellc
A;Reference number: A42452; MUID:92188538; PMID:1546458
A;Accession: A42452
A;Molecule type: DNA
A;Residues: 1-102 < MOR>
A;Residues: 1-102 < MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rikomatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
Apittle: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate syntha
A;Reference number: S72648; MUID:96439842; PMID:8842155
A;Accession: S72649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose A, Pathway: sucrose blosynthesis
(S. Superfamaily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C, Keywords: glycosyltransferase; hexosyltransferase; sucrose-blosynthesis
F;1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <8SPS>
A;Molecule type: DNA
A;Reaidues: 1-363 <KLE>
A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule Trype: MANA A; Residues: 1-341 «KDNA A; Residues: Experimental Bource: Erult, cv. Miyagawa-Wase A; Resperimental Bource: Erult, cv. Miyagawa-Wase C; Residues: Resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
C;Species: Citrus unshiu
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: S72649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V1 protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2; Length 341;
Pred. No. 16;
2; Mismatches 1; Indels
                                                                                                                                                                   Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 2;
Pred. No. 4.3;
3; Mismatches ::
                                                                                                                                                                        DB 2;
                                                                                                                                                                   Score 38; DB;
Pred. No. 6.8;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%;
ilarity 60.0%;
Conservative 3
                                                                                                                                                                   Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 120 ENIVPYGIDFS 130
                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||| |::||
7 QVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| |||:|
228 VIPPGMDFS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

Best Loc Matches

ð g RESULT 4

ö

Gaps

ö

ö

Gaps

ö

RESULT 5

ò 셤

```
Sucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
C; Accession: T04062
R; Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F submitted to the Protein Sequence Database, March 1999
A; Reference number: Z15184
A; Accession: T04062
A; Molecule type: DNA
A; Residuae: 1-1083 - SEV->
A; Molecule type: DNA
A; Residuae: 1-1083 - SEV->
A; Experimental source: cultivar Columbia; BAC clone F28M11
C; Genetics:
A; Map position: 4
A; Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3;
A; Note: F28M11.40
C; Superfamily: sucrose-phosphate synthase homology
Plant Physiol. 115, 113-121, 1997

A;Title: Analysis of CDNA clones encoding sucrose-phosphate synthase in relation to su A; Reference number: Z16874; MUID:97451773; PMID:9306694

A;Accession: T09837

A;Accession: T09837

A;Accession: T09837

A;Acsidues: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1081 < ING>
A;Cross-references: EMBL:Y11795; NID:92190349; PIDN:CAA72491.1; PID:92190350
A;Experimental source: ABA-treated callus
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: giycosyltransferase; hexosyltransferase; sucrose biosynthesis
P;176-674/Domain: sucrose/sucrose-phosphate synthase homology <SSS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Oryza sativa (rice)
C;Dace: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Dacession: T04103
R;Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T.
Plant Sci. 112, 207-217, 1995
A;Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene
A;Reference number: 215212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: sucrose-pnospnare synchase, corrections (SSPS) F;230-714/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 2; Length 1081; Pred. No. 60; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Score 36; DB 2; Length 1083; 66.7%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T04103
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1084 <SAK>
A;Crose-references: EMBL:D45890; PIDN:BAA08304.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: subsp. Japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| |||:|
445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:| |||:|
483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-1049 < VAL>
A; Cross-references: GB: MID: g1449931; PIDN: AAC49379.1; PID: g988270
A; Note: UPEQ! ucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDEglucosylt
C; Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
C; Genetics:
A; Gene: Sps1
A; Introns: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sucrose-phosphate synthase (EC 2.4.1.14) - maize
Sucrose-phosphate synthase (EC 2.4.1.14) - maize
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JQ1329; PQ0260
R;Worrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
Baint Cell 3, 112-1130, 1991
A;Title: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd
A;Reference number: JQ1329; MUID:92338837; PMID:1840396
C;Date: 10-May-1996 #8equence_revision 16-Aug-1996 #text_change 18-Jun-1999
C;Accession: JC4783
R;Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella Gene 170, 217-222, 1996
A;Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
A;Reference number: JC4783; MUID:96235138; PMID:8666248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc A;Pathway: sucrose biosynthesis
(S.Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; haxosyltransferase; sucrose biosynthesis
F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 71-74;206-212;471-481;872-892 <WOR1>
C; Comment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-phosph
C; Comment: This enzyme is involved in the regulation of carbon partitioning in the leave
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology C;Reywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis F;178-666/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Cpate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: T09837 R;Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1068 <WOR>
A;Cross-references: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 1049;
Pred. No. 58;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1
Pred. No. 59;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 66.7%;
Similarity 66.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pathway: sucrose biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:| |||:|
436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: PQ0260
                                                                                                                                                                                                                                                                         Accession: JC4783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: JQ1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              쉽
```

ţ

ò 셤

```
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: H72784
R;Kawarabayasi, Y:; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taki
Bwa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. G, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: H72184
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 «KAM»
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79178.1; PID:g5103657
A;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
R;Mortimore to the EMBL Data Library, November 1996
A;Reference number: 21923
A;Reference number: 21933
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mortimore and Caenories and Caenor
                                                                                                                                     probable alkaline proteinase APE0263 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 2
Pred. No. 35;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: APE0263
C;Superfamily: subtilisin; subtilisin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| |:|||
562 VLPVGIDYS 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 EVLPWGVDY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
Cipecies Caulobacter crescentus
Cipecies Caulobacter crescentus
Cibate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
CiAccession: H87660
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Li Ermolaeva, M.: White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: preliminary
                                                                    A;Map position: 1
A;Map position: 1
A;Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltranaferase; hexosyltranaferase
F;196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ripercy, C. submitted to the EMBL Data Library, October 1996
submitted to the EMBL Data Library, October 1996
A.Reference number: 219842
A.Acession: T24111
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-425 <WIL>
A.Cross-references: EMBL: Z81109; PIDN: CAB03241.1; GSPDB: GN00023; CESP:R10D12.10
A.Experimental source: clone R10D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-433 <STO>
A;Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC3322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                             Length 1084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 2; Length 433;
Pred. No. 34;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 425;
                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein R10D12.10 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                          Score 36; DB 2;
Pred. No. 60;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.8%; Score 35; DB Best Local Similarity 50.0%; Pred. No. 34; Matches 5; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 23/3; 56/3; 113/3; 257/2
                                                                                                                                                                                                                                                                                          66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 EVILPPGFDYS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 EQIVPGGLQY 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| |||:|
453 VIPPGMDFS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP:R10D12.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: T24111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 5
C;Genetics:
A;Gene: Sps1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

Gaps

ö

1; Indels

Length 440;

```
A;Gene: CBSP:C53A5.2
A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Rimatthews, L.
submitted to the EMBL Data Library, August 1996
A; Reference number: Z19808
A; Reference number: Z19808
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rotecule type: DNA
A; Residues: 1-1150 < WIZ>
A; Cross-references: EMBL: Z78015; PIDN: CAB01437.1; GSPDB: GN00023; CESP: C53A5.2
A; Experimental source: clone R02D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                            Length 1150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   64.8%; Score 35; DB 2;
llarity 66.7%; Pred. No. 1e+02;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: December 22, 2003, 17:44:58 Job time : 10.0667 secs
```

```
Q8rg86 fusobacteri
P31619 tobacco yel
Q43802 oryza sativ
P31927 cea mays (m
D04933 craterostig
P8284 drosophila
Q9nr64 homo sapien
P20423 oryza sativ
P08248 hordeum vul
P11970 populus nig
P94283 borrelia bu
Q9f48 arabidopsis
Q9w419 arabidopsis
Q9w419 arabidopsis
Q9w419 arabidopsis
Q9w419 arabidopsis
Q9w34 wibrio chol
P08503 rattus norv
Q9cau7 homo sapien
Q61851 mus musculu
P18460 gallus gall
Q74377 schizosacch
P1862 homo sapien
Q9kv29 vibrio chol
P1882 homo sapien
Q9kv29 vibrio chol
P1882 homo sapien
Q9kv29 vibrio chol
P19102 xenopus lae
                                                                                                                         December 22, 2003, 16:43:51; Search time 4.6 Seconds (without alignments) 112.455 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                        127863
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                          127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARB FUSINI
SPS ORYSA
SPS ORYSA
SPS MAIZE
SPS CRAPL
PAP DROWE
KHLI HIWAN
PLAS ORYSA
PLAS HORYU
SYFB BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R8L4_ARATH
RPRPB_ARATH
RPRPB_ARATH
Y939_METUA
Y939_METUA
HWAN_PERAR
HWAN_PERAR
ACDM_RAT
ACDM_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                     US-09-909-164-13
                                                                                                                                                                                                                                                            1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SwissProt_41:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    666.77
669.30
693.90
693.00
693.00
693.00
693.00
693.00
693.00
                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                       Perfect score:
                                                                                  OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
```

| 34 32 59.3 231 11 ARAD SALITY 35 32 29.3 288 1 CGDD_HUMAN 36 32 59.3 288 1 CGDD_HUMAN 36 32 59.3 289 1 CGDD_HUMAN 38 32 59.3 289 1 CGDD_HUMAN 40 32 59.3 291 1 CGDD_HUMAN 41 32 59.3 291 1 CGDD_CGTC 42 59.3 291 1 CGDD_CGTC 43 25.3 291 1 CGDD_CGTC 44 12 59.3 291 1 CGDD_HUMAN 45 12 59.3 291 1 CGDD_HUMAN 46 12 59.3 291 1 CGDD_HUMAN 47 12 59.3 291 1 CGDD_HUMAN 48 12 59.3 291 1 CGDD_HUMAN 49 12 59.3 291 1 CGDD_HUMAN 40 12 59.3 291 1 CGD_HUMAN 40 12 59.3 291 1 CGDD_HUMAN 40 12 59.3 291 2 CGDD_HUMAN 40 12 59.3 | P06190 salmonella Q9wzrl thermotoga Q04827 rattus norv P30279 homo sapien P30280 mus musculu Q90459 brachydanio P50755 xenopus lae P43706 gallus gall P53782 xenopus lae P55169 gallus gall P30281 homo sapien P24385 homo sapien | nnce update) cation u | atics and the EWB here are no restria as its content i d. Usage by and e http://www.isb-si |
|--|---|--|--|
| 34 32 59.3 231 1 ARM 35 32 59.3 231 1 HISS 36 32 59.3 288 1 CGD 39 32 59.3 289 1 CGD 39 32 59.3 289 1 CGD 40 32 59.3 291 1 CGD 41 32 59.3 291 1 CGD 42 32 59.3 291 1 CGD 43 32 59.3 291 1 CGD 43 32 59.3 291 1 CGD 44 32 59.3 291 1 CGD 45 32 59.3 291 1 CGD 45 32 59.3 291 1 CGD 46 32 59.3 291 1 CGD 47 32 59.3 291 1 CGD 48 58 FUSNN STANDARD; FR CARB OR FN0422. PUSODACTETION M. A. BATHARD; RE PUSODACTETION M. A. BATHARA STANDARD; REDLINB-21886394; PubMed-118891(Kapatral V., Anderson I., Ivanov BACTERION N. A. BATHARA STANDARD SEQUENCE FROM N. A. STRAIN-ATCC 25586; [1] SEGUENCE FROM N. A. STRAIN-ATCC 25586; MEDLINB-21886394; PubMed-118891(Kapatral V., Anderson I., Ivanov BACTERION M. Kyrpides N., Overb WEDLINB-21886394; PubMed-118891(Kapatral V., Anderson I., Ivanov BACTERION M. A. STRAIN-ATCC 25586; MEDLINB-2186394; PubMed-118891(Kapatral V., Anderson I., Ivanov BACTERION M. A. STRAIN-ATCC 25586; MEDLINB-2186394; PubMed-118891(Kapatral V., Anderson I., Ivanov BACTERION M. A. STRAIN-ATCC 25586; MEDLINB-2186394; PubMed-118891(Kapatral V., Anderson I., Ivanov BACTERION M. A. STRAIN-ATCC 25586; MEDLINB-2186394; PubMed-118891(Kapatral V., Anderson I., Ivanov BACTERION M. A. STRAIN-ATCC 25586; MEDLINB-2186394; PubMed-118891(Kapatral V., Anderson I., Ivanov BACTERION M. A. STRAIN-ATCC 25586; MEDLINB-2186394; PubMed-118891(Kapatral V., Anderson I., Ivanov BACTERION M. A. STRAIN-ATCC 25586; MEDLINB-218630504; Compation of two che between the Swiss Institute of the Buropean Bioinformatics Institution modified and this statement is rentities requires a license agree This SWISS-FROY The Province IPRO0549; CPase-I. The Province IPRO0549; CP | LTY EMA MAN USB ARB NLA ICK MAN MAN | upd con upd co | reado reado con con con con con con con con con con |
| 34 32 59.3 231 1 ARM 35 32 59.3 231 1 HISS 36 32 59.3 288 1 CGDD 39 32 59.3 289 1 CGDD 39 32 59.3 289 1 CGDD 40 32 59.3 291 1 CGDD 41 32 59.3 291 1 CGDD 42 32 59.3 291 1 CGDD 43 32 59.3 291 1 CGDD 43 32 59.3 291 1 CGDD 44 32 59.3 291 1 CGDD 45 32 59.3 291 1 CGDD 45 32 59.3 291 1 CGDD 46 32 59.3 291 1 CGDD 47 32 59.3 291 1 CGDD 48 59.3 292 1 CGDD 28 FEBS-2003 (Rel. 41, Last seque 38 FEBS-2003 (Rel. 41, Last seque 39 FEBS-2003 (Rel. 41, Last seque 39 FEBS-2003 (Rel. 41, Last seque 30 FEBS-2003 (Rel. 41, L | | TT; in the property of the pr | INIT ALL STREET |
| 8 8 E | ARAL HISS CGD CGD CGD CGD CGD CGD | Present of the presen | ALT ALT 1. 22. 22. 22. 22. 22. 22. 22. 22. 22. |
| 8 8 E | | eat te passes te passes te passes te passes to | trucker trucker trucker trucker nase trucker t |
| 8 8 E | 20011000000000000000000000000000000000 | ANDARD; 41, Cr 41, La 41, Cr 41, La 80 80 80 80 80 80 80 80 80 80 80 80 80 | a Institution of the control of the |
| 8 8 E | | ST ST ST ST ST ST ST ST ST ST | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 |
| 8 8 E | | 33 (F 13 (F 14 (F 15 (F 15 (F 16 | he is a second of the is a secon |
| 8 8 E | 00000000000000000000000000000000000000 | SNN RGB FUSNN RGB 70 FFBB-200 | Marian Indian In |
| O) EL | W W W W W W W W W W W W W W W W W W W | | President in the president of the presid |
| | | on ex | |

listeria in listeria mo rattus norv escherichia

Q04667 P08203

RAT ECOLI

```
7 QVVPSGINYS 16
                                                                                       ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
SPS MAIZE
                                                               RESULT 3
SPS ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                   ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                         윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                            ô
PERM; PF02142; MGS; 1.

DR PRINTS; PR00098; CPSASE.

DR PROSITE; PS00866; CPSASE.12.

DR PROSITE; PS00866; CPSASE.2; 2.

DR PROSITE; PS00867; CPSASE.2; 2.

KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Complete protecome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

402 546 CARBAMONL PHOSPHATE SYNTHETIC DOMAIN.

CARBAMONL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-2918853B, PubMed=154645B;
MORTISE 9.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.B.;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.B.;
The nucleotide sequence of the infectious cloned DNA component of
Tobacco Pallow dwarf virus reveals features of geminiviruses
infecting monocotyledonus plants.";
Virology 187:633-642(1992).
                                                                                                                                                                                                                           2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                    210 ATP (POTENTIAL).
284 MANGANESE 1 (BY SIMILARITY).
298 MANGANESE 1 (BY SIMILARITY).
300 MANGANESE 2 (BY SIMILARITY).
820 MANGANESE 2 (BY SIMILARITY).
821 MANGANESE 3 (BY SIMILARITY).
832 MANGANESE 3 (BY SIMILARITY).
117451 MM, ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                  Score 38; DB 1; Length 1058;
Pred. No. 9.1;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 60.0%; Pred. No. 2;
6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  il protein. -
102 Aa; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR02521; Gemini mov. Pfam; PF01708; Gemini mov; I. Hypothetical protein. SEQUENCE 102 AA; 11178 MW; A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-OTJ-1993 (Rel. 27, Last ann
Hypochetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                   70.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                               6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                   2 EVVPXGMDYS 11
                                                                                                                                                                                                                                                                            058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; seDNA vi
                                                                                                                                                                                                                                                                                                                                                                                                                            YIIK TYDVA
ID YIIK TYDVA
AC P31619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                          REPEAT
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

EVVPXGMDYS 11

ò

:: =

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BUCTOBE 6-PROBPHAGE.

-I-ENEYME REGULATION AND
MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.

-I-PATHWAY: Sucrose synthesis.

-I-SUBUNIT: Homodimer or homotetramer (By similarity).

-I-PATHWAY: HOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).

-I-SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.
-i- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Straptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herrera-Estrella L.; "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 36; DB 1; Length 1049; 66.7%; Pred. No. 24; ive 2; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      775 779 POLY-ARG.
1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. Indica-IR36; TISSUB=Leaf;
MEDLINE=96235138; PubMed=8666248;
Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-Phosphate synthase (EC 2.4.1.14)
(UDP-glucose-fructose-phosphate glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1068 AA.
PRT; 1049 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPS MAIZE STANDARD;
P31927;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U33175; AAC49379.1; -. PIR; JC4783; JC4783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 66.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene.";
Gene 170:217-222(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMDYS 11
                                                                                                                                                                                                                      Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
```

ψ.

```
Asteridae, lamiids, Lamiales, Lamiales incertae sedis, Torenieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fischer-Vize J.A., Rubin G.M., Lehmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Bye imaginal disk;
MEDLINE=93202020; PubMed=1295747;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y11795; CAA72491.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 66.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:| |||:|
445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDYS
                         NCBI TaxID=4153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                               STRAIN=CV. PIONEER 3184; TISSUE=Leaf;
MEDLINE=92338837; PubMed=1840396;
Worrell A.C., Bruneau J.-M., Summerfelt K., Boersig M., Voelker T.A.;
"Expression of a maize sucrose phosphate synthase in tomato alters
leaf carbohydrate partitioning.";
Plant Cell 3:1121-1130(1991).
-!- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREFORE PLAY A MAJON ROLLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
-!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craterostigma plantagineum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last anotation update)
Sucrose-phosphate synthase 2 (RC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase 2).
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
                                                                                                                                      SEQUENCE PROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                      ENZYME FUNCTION.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR001296; Glyco trans 1.
Pfam; PF00534; Glycos transf 1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1081 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLY
                                      phosphate glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M97550; AAA33513.1; -. PIR; JQ1329; JQ1329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 VIPPGMDPS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                             NCBI_TaxID=4577;
                                                               Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JQ1329; JQ1
MaizeDB; 25294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         004933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPS2_CRAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPS2
                                                                                                                                                                                                                                                                                                                                                                                                    +
 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUCKOSE 6-PROSPHATE.

-I-ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF WETABOLITES AND LIGHT.

-I-PATHWAY: SUCTOSE SYNTHESIS.
-I-SUBLWAIT: HOMODIMET OF HOMOCETERE (By similarity).
-I-THM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
-I-SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                              Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.;
"Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to sugar interconversions associated with dehydration in the resurrection plant Craterostigma plantagineum Hochst.";
Plant Physiol. 115:113-121(1997).
-!- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREPORE PLAY A MAJOR ROLE AS A LIMITING PACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.
-!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P55824; Q9V976; Q7V027;
01-NOV-1997 (Rel. 35, Created)
28-F8B-2003 (Rel. 35, Created)
28-F8B-2003 (Rel. 41, Last sequence update)
28-F8B-2003 (Rel. 41, Last sequence update)
Probable ubiquitin carboxyl-terminal hydrolase PAF (EC 3.1.2.15)
Probable ubiquitin carboxyl-terminal hydrolase PAF (EC 3.1.2.15)
Probable ubiquitin carboxyl-terminal hydrolase PAF (EC 3.1.2.15)
Probable ubiquiting enzyme PAF) (Ubiquitin-specific processing protease PAF) (Deubiquitinating enzyme PAF) (Ubiquitin-specific processing protease PAF) OR BCDNA:LD22582 OR CG1945.
Drosophila melanogaster (Fruit fly).
BNARYOCA: Metazzoa; Arthropoda; Hexapoda; Insecta; Pterygota;
PROPERTA: Endopterygota; Diptera; Brachycera; Muscomorpha;
PNCBI_TAXID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Glycosyltransferase; Phosphorylation; Multigene family. DOMAIN 245 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Score 36; DB 1; Length 1081; 66.7%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 2778 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; T09837; T09837.
InterPro; IPR001296; Glyco_trang_1.
Pfam; PF00534; Glycog_transf_1; 1.
SEQUENCE PROM N.A. MEDLINE-97451773; Pubmed-9306694;
```

COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR

```
RA Adams W.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D., Ramanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E. Richards S. Ashburner M., Henderson S.N., Sutton G.G., Wortwas D.E. Richards S. Ashburner M., Henderson S.N., George R.A., Lewis S.E. Richards S., Ashburner M., Henderson S.N., Bruton G.G., Wortwas D.E., Baxer R.G., Chango Q., Chen L.X., RA Andrews Peanhoch C., Baldwin D., Raman B.L., Banden R.C., Baseley E.M., Ballew R.W., Basu A., Barena B.P., Bhandari D., Bolshakov S., Ballew R.Y., Benos P.V., Barman B.P., Bhandari D., Bolshakov S., Ballew R.C., Bucchan M.R., Bouck J., Broketein P., Brottler P., Brottler P., Botchan M.R., Bouck J., Browenport L.B., Davies P., Ra Dethors B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dedson K., Doup L.E., Downes M., Dudan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dudan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dudan-Rocha S., Dunkov B.C., Dunn P., Roder C., Gabrielian A. S., Gargan P., Harries M.C., Gabrielian A. K.G., Gargar M.-H., Ibegwam C., Gabrielian A. K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Harris M.L., Harvey D., Helman T.J., Weil M.-H., Ibegwam C., Jalali M., Kalush P., Karpen G.H., Kez J. Kennison J.A., Ketchum X.A., Jalali M., Kalush P., Karpen G.H., Kez J., Kennison J.A., Moshrefi A., Month S.M., Month S.M., Mishina N.V., Moharry C., Morris J., Moshrefi A., Mohary C., Morris J., Musham D.L., Merkulov G., Milbhina N.V., Moharry C., Morris J., Puri V., Renington K.A., Nixon K., Nusseern D., Mrisham S., Shue B.C., Siden-Kamos I., Simpson M., Strong R., Sun B., Spier E., Spradling A.C., Stapleton M., Stupki M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Wang Z.-Y., Wassarman D.A., Wainstock G.M., Weissenbach J., Puri Wang Z.-Y., Wassarman D.A., Wainstock G.W. D., Puri V., Santh H.O., Spier E., Spradling A.C., Stapleton M., Stupki M., Puller S., Shen B.C., Stan-Kamos I., Simpson M., Stupki M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
MEDLINE=20196012; PubMed=10731138;
MEDLINE=20196012; PubMed=10731138;
Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,
Stapleton M., Harvey D.A.;
"A Drosophila complementary DNA resource.";
Science 287:222-2224(1000).
-!- FUNCTION: REQUIRED FOR EYE AND EMBRYO DEVELOPMENT, AND PLAYS A
ROLE IN COMPOUND BYE ASSEMBLY AND COGENESIS RESPECTIVELY. IN THE
LARVAL BYE DISKS, CELLS OUTSIDE THE ASSEMBLING FACETS REQUIRE THIS
PROTEIN FOR SHORT-RANGE CELL INTERACTIONS THAT PREVENT THE MYSTERY
CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR
NUCLEAR MIGRATION AND CELLULARIZATION IN EARLY EMBRYOGENESIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P. Bettenocut B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Annotation of the Drosophila melanogaster euchromatic genome: a
The fat facets gene is required for Drosophila eye and embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
MEDLINE=22426069; PubMed=12537572;
                                                                                                                          STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                Development 116:985-1000(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systematic review.";
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ξ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0005632; faf.

GO; GO:0005734; C:cytcplasm; IDA.
GO; GO:0007349; P:emcllularization; IMP.
GO; GO:0007349; P:emcllularization; IMP.
GO; GO:0008783; P:emcllularization; IMP.
GO; GO:0008583; P:mystery cell fate differentiation (sensu Dr. . .; IMP.
GO; GO:0006512; P:ubiquitin cycle; IGI.
InterPro; IPR001394; UCH-2.
FROM: PF00443; UCH-2.
FROM: FS00972; UCH-2.
FROM: FS00973; UCH-2.; I.
FROSITE; FS00973; UCH-2.; I.
FROSITE; FS00973; UCH-2.; I.
FROSITE; FS00973; UCH-2.; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubl conjugation pathway; Hydrolase; Thiol protesse;
Developmental protein; Vision; Alternative splicing.
ACT SITE 1677 1677 BY SIMILARITY.
ACT SITE 1978 1978 BY SIMILARITY.
ACT SITE 1986 1986 BY SIMILARITY.
ACT SITE 1986 1986 BY SIMILARITY.
ARREPLIC 2705 2778 KRRWILIKULVESKDEBATTATTAATTEVTTSPATAIATA
ATLEPAGMSELITWVEKNLIISQENPQAKSSLQ. -> VTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                           Isoid=P55824-3; Sequence=VSP 005269;
TISSUE SPECIFICITY: EYE DISKS AND OVARIES.
DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
SIMILARITY: Belongs to peptidase family C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IATAATLEPĀGMSELTTMVEKNLIISQENPQAKSSLQ
SQRQQL (in isoform 2).
               FUNCTION.

CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
                                                                    Bvent=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E -> D (IN REF. 1).
T -> S (IN REF. 1; AAF01345)
MW; FFB90438BA53A02B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNV (in 1soform 3).
/FTId=VSP_005269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 1; 1
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             005270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                IsoId=P55824-2; Sequence=VSP_005270;
                                                                                                                                   IsoId=P55824-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                           234 234
2725 2725
2778 AA; 311139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.5.,
6; Conservative
                                         ubiquitin + a thiol.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2742
                                                                                                                       Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
```

| :|| | |:| 1394 EVIVPDGQDFS 1404 1 REVVPXGMDYS 11

용 Š

KHL1_HUMAN

RESULT 7

ä

Gaps

;

Indels

ö

80.0%; Pred. No. 34; ive 1; Mismatches

1 BEVVPXGMDY 10

```
Best Local Similarity 80.0
Matches 8, Conservative
                                                                                                         127 EEVVP-GMDF 135
                                                                                                                                                                                             PLAS_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                    ð
                                                                                                         셤
                                                                                                                                                                                                                                       $\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
MEDLINE-20277482; PubMed-10819331;
Megase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Negase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XVII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 605332; -. 605032; -. 605032; -. 60500377; P.actin binding activity; NAS. 60:00037036; P.actin cytoskeleton organization and biogenesis; NAS. InterPro; IPR000210; BTB_PO2. InterPro; IPR006522; Kelch_rep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
THE BRAIN CELLS.
                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=20347694; PubMed=10888605;
Koob M.D., Nemes J.P., Benzow K.A.;
"The SCAS transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI).";
Hum. Mol. Genet. 9:1543-1551 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C11C43D8282F9FF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Highly expressed in brain.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
-!- SIMILARITY: Contains 6 Kelch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kelch repeat; Repeat.
SER-RICH.
                 O9NR64; Q9H4X4; Q9NR65; Q9P218;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Kelch-1ike protein 1.
Kelch-1ike protein 1.
Homo sapiens (Human)
  748 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF252283; AAF81719.1; --
EMBL, AF252279; AAF81716.1; --
EMBL, AB040923; BAA96014.1; --
EMBL, AL353738; CAC16128.1; --
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00651; BTB; 1.
Pfam; PF01344; Kelch; 6.
SMART; SM00225; BTB; 1.
SMART; SM0612; Kelch; 6.
PROSITE; PS50097; BTB; 1.
Cytoskeleton; Actin-binding; Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82680 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 179-409 FROM N.A.
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:6352; KLHL1.
MIM; 605332; -.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           748 AA;
                                                                                                                                                                                                                 NCBI_TaxID=9606;
  KHL1 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay
```

DB 1; Length 748;

Score 34.5;

63.9%;

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               Lee J.-8.; "Molecular cloning and characterization of plastocyanin precursor in
                                                                                                                                                                                                                      Bukaryota, Viridipiantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BTRAIN=CV. Japonica;
MEDLINE=89386623; PubMed=2780537;
Yano H., Kamo M., Tsugita A., Aso K., Nozu Y.;
The Amino and sequence of plastocyanin from rice (Oryza sativa, subspecies japonica).";
Protein Seq. Data Anal. 2:385-389(1989).
I- FUNCTION: Participaeta in electron transfer between P700 and toytochrome b6-f complex in photosystem I.
I- SUBCELLUIAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURPACE IN CHICNROPLASTS.
I- SIMILARITY: Contains I plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000923; BlueCu 1.
InterPro; IPR000923; BlueCu 1.
InterPro; IPR001925; Copper_blue.
Pram; PR00127; copper-bind; 1.
ProDom; PD001235; Copper blue; 1.
PROSITE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane; Transit peptide. 57 CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 PLASTOCYANIN.
154 PLASTOCYANIN.
154 COPPER (BY SIMILARITY).
139 COPPER (BY SIMILARITY).
147 COPPER (BY SIMILARITY).
147 COPPER (BY SIMILARITY).
147 COPPER (BY SIMILARITY).
15577 MW; 845725D25B5F400D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
PLAS ORYSA STANDARD; PRT; 154 AA. P20423; Q9SBB8; 01-F8B-1991 (Rel. 17, Created) 28-FRB-2003 (Rel. 41, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=CV. Ilpoom; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF093636; AAC78108.1; -. HSSP; P00289; 2PCF. Gramene; P20423; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
1154
1154
1139
1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
58
139
139
142
147
154 AA;
                                                                                                                                                                                                   Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 58-154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rice."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
```

Pred. No. 8.2;

54.5%;

```
6; Conservative
Best Local Similarity
                                                                                                      PLAT POPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRTAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                               RESULT 10
PLAT_POPNI
           Matches
                                                                                                                 ò
                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
ö
                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
STRAIN=CV. NK 1558;
MEDLINE=94039081; PubMed=8223592;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
Gaps
                                                                                                                                                                                                                                                                                                                                                            promoter region.";

Eur. J. Biochem. 217:97-104(1993).

-!- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-!- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURPACE IN CHLOROPLASTS.
                                                                                                                                                                Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                         STRAIN=cv. Bomi;
Nielsen O.S., Gausing K.;
"The precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues.";
PEBS Lett. 225:159-162(1987).
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y00704; CAA68696.1; -.
EMBL; Z28347; CAA82201.1; -.
PIR; S38255; S3825.
INTERPO; PR001235; COPPET_blue.
Pfam; PR00127; COPPET_blue.
Pfam; PR00127; COPPET_blue.
Promo; PR00123; COPPET_blue.
PRINTS; PR00123; COPPERBLUE.
PROSTTE; PS00194; COPPER BLUE.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
T -> N (IN CV. NK 1558).
W; DAATZABESF6F4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 plastocyanin-like domain.
3;
                                                                                                                          Last sequence update)
Last annotation update)
                                                                                            155 AA
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLASTOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLOROPLAST
                                                                                                                                               Plastocyanin, chloroplast precursor.
5
                                                                                                               (Rel. 08, Created)
(Rel. 08, Last seqn
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MΨ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15709
Conservative
                                                                                            STANDARD;
                                        100 EDAVPSGVDVS 110
                    1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
148
120
155 AA;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fransit peptide
                                                                                                                01-AUG-1988
                                                                                                                          01-AUG-1988
28-FEB-2003
. 9
                                                                                           PLAS HORVU
P08248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                   PLAS_HORVU
Matches
                                                                        RESULT
                                                                                                     a
                    ઠે
```

DB 1; Length 155;

Score 34;

63.0%;

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Malpighiales, Salicaceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIMILETON II. BGOTOVO C.A., Donchev A.A., Atanasov B.P.;
Dimiletov M.I., EGOTOVO C.A., Donchev A.A., Atanasov B.P.;
FEBS Lett. 226:17-22(1987).
-I- FUNCTION: Participates in electron transfer between P700 and the cytochrome be-f complex in photosystem I.
-I- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHIOROPLASTS.
-I- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYDAINS AND B.
-I- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Gape
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probom; PD01235; Copper blue; 1.
PROSITE; PS00196; COPPER BLUE; 1.
Chloroplast; Blectron transport; Copper; Thylakoid; Membrane;
Transit peptide; Multigene family.
TRANSIT 1 69 PLASTOCYANIN B.
CHAIN 70 168 PLASTOCYANIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.0%; Score 34; DB 1; Length 168; 54.5%; Pred. No. 8.9; ive 2; Mismatches 3; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=cv. Italica; TISSUB=Leaf;
STChert J., Janzel-bewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPPER.
P20DA6BA2038ABBA CRC64;
3,
                                                                                                                                                                                                                                                                                                  (Rel. 12, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                   168 AA
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Plastocyanin B, chloroplast precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COPPER.
COPPER.
COPPER.
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P00299, IPLC.
INTERPO, IPR000923; BlueCu 1.
InterPo, IPR001235; Copper_blue.
Pfam; PP00127; copper_bind; 1.
PRINTS; PR00156; COPPERBIUE.
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Populus nigra (Lombardy poplar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z50186; CAA90565.1; -. PIR; S00210; S00210. PIR; S58208; S58208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                       |: || |:| |
101 EDAVPSGVDVS 111
                                                                                                                                                                                                                                                   STANDARD;
                                                       1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 70-168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3691;
                                                                                                                                                                                                                                                                                                  01-OCT-1989 (
01-OCT-1996 (
28-FRB-2003 (
```

ઠ 윱

us-09-909-164-13.rsp

```
ద
          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                      28-FEB-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (RC 6.1.1.20) (Phenylalanine--
tRNA ligase beta chain) (PheRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98065943; PubMed=9403685; Rasar C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Dougherty B., Tomb J.P., Felstchmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., Van Wugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03484; B5; 1.
TIGRFAMs; TIGR00471; pheT_arch; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A.
SEQUENCE ASC. 4 Hinnebusch J.;
Barbour A.G., Hinnebusch J.;
Barbour A.G., Hinnebusch J.;
Phenylalanyl-tRNA synthetase genes (alpha and beta subunits) and "Phenylalanyl-tRNA synthetase gene of Borrelia burgdorferi.";
thioredoxin reductase gene of Borrelia burgdorferi.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP + diphosphate + L-phenylalanyl-tRNA(Phe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA
CHAIN FAMILY. SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.0%; Score 34; DB 1; Length 566; 85.7%; Pred. No. 32; 1; Indels 1; Indels

    -1- SUBUNIT: Tetramer of two alpha and two beta chains (By

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAWAP, MF 00284; -; 1.
InterPro; IPR005147; B5.
InterPro; IPR004531; PheT_arch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U82978; AAB41019.1; -.
EMBL, AR001153; AAC66870.1; -.
PIR, A70164; A70164.
TIGR, BB0514; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:580-586(1997).
                                              |: || |:| |
112 BDAVPSGVDVS 122
                                                                                                                                                                                                                                               STANDARD;
1 BEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          burgdorferi
                                                                                                                                                                                                                                           BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                           SYFB_BORBU
```

ö

Gapa

ö

6; Conservative

Best Local Similarity

Matches

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: Contains 3 leucine-rich (LRR) repeats.
-1- SIMILARITY: Contains 1 NB-ARC domain.
-1- DATABASE: NAME-NIB-LRRS;
NOTE-Runctional and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.

STRAIN=cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Potential disease resistance protein.
-I- DOMAIN: The LRR repeats probably act as specificity determinant of pathogen recognition (By similarity).
-I- SIMILARITY: Belongs to the disease resistance NB-LRR family.
                                                                                                                                                             15-58P-2003 (Rel. 42, Last amotation update)
15-58P-2003 (Rel. 42, Last amotation update)
Probable disease resistance RPP8-like protein 4.
RPP8L4 OR AT5G48620 OR K15N18.9.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids III Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRATN=cv. Columbia,
MEDLINE-99087489; PubMed-9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRR 1.
LRR 2.
LRR 3.
ATP (POTENTIAL).
                                                                                                                    908 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB015468; BAB10695.1; -.
EMBL; AX13163; BAC41841.1; -.
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR001811; LRR.
Pfam; PP00560; LRR; 2.
Pfam; PP00931; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homologs;
WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NB-ARC.
                                                                                                                                                    (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 5:297-308(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPP8/HRT subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45
45
59
623
623
867
                   || ||||
169 VPPGMDY 175
4 VPXGMDY 10
                                                                                                                                                                                                                                                                                                  NCBI TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
146
575
600
                                                                                                                                                 15-SEP-2003
                                                                                                                  RBL4 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                            Tabata S.;
                                                                                                                                 Q9PJK8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
```

```
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RBPBAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cooley M.B., Pathirana S., Wu H.-J., Kachroo P., Klessig D.F.; "Members of the Arabidopsia HRT/RPP8 family of resistance genes confer resistance to both viral and comycete pathogens."; Plant Cell 12:663-676(2000).
                                                                                                                                                                                                                                                                                                                                                                      Holub B.B., Dangl J.L.,
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                      RPPB ARATH STANDARD; PRT; 908 AA.
QBW4J9; QBGWG5; Q9M5A1; Q92SY3; Q92SY4;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
D15-SEP-2003 (Rel. 42, Last annotation update)
D15-SEP-2003 (Rel. 42, Last annotation update)
D15-SEP-2003 (Rel. 42)
                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae;
eurosida II, Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
                                              Gaps
                                                                                                                                                                                                                                                                                                               (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato S., Nakamura Y., Kaneko T., Katoh T., Abamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 RPP8-1, AND VARIANTS.
STRAIN-CV. Columbia, and cv. Landsberg erecta;
MEDLINE=99030133; PubMed=9811794;
MCDOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced is consortium (Salk/Stanford/PGEC).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                      Score 34; DB 1; Length 908;
Pred. No. 53;
                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayaahizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length CDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
104448 MW; 3111991B17239693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS
                                             2; Mismatches
                                                                                                                                                                                                                    RPP8 OR HRT OR AT5G43470 OR MWF20.19
Arabidopsis thaliana (Mouse-ear crees
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Di-17;
MEDLINE=20271766; PubMed=10810142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [6]
INTERACTION WITH TIP.
MEDLINE-20496823; Pubmed=11041886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Cell 10:1861-1874(1998).
                      63.0%;
           Query Match
Best Local Similarity 60...
                                                                                           883 EKLVPGGEDY 892
                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 7:31-63(2000)
                                                                    BEVVPXGMDY
 908 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                     -
 SEQUENCE
                                                                                                                                        RPP8_ARATH
                                                                                                                            RESULT 13
 စ္တ
                                                                                                                                                           ઠે
                                                                                         셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE-Functional and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note=Has been shown to exist only in cv. Columbia so far;
Note=Has been shown to exist only in cv. Columbia so far;
Note=Has been shown to exist only in cv. Columbia so far;
DOMAIN: The LRR repeats probably act as specificity determinant of
pathogen recognition.

POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and
cv. Columbia are probably due to an unequal crossing-over between
the highly related RPPs and RPHsA genes present in cv. Landsberg
erecta. Such variations probably modify the specificity of
                                                                                                                the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. The interaction with TIP (TCV-interacting protein) may be essential for the recognition of the avirulence proteins, and the triggering of the
Ren T., Qu F., Morris T.J.;
"HRT gene function requires interaction between a NAC protein and
"viral capsid protein to confer resistance to turnip crinkle virus.";
Plant Cell 12:1917-1926(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WROMLITSRNEGVGIH -> ELLWYIHEALFLINS (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erecta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat;
Alternative splicing; Polymorphism.
DOMAIN 145

LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogen recognition.
MISCELLANEOUS: In cv. Columbia and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP 007171.
Missing (In isoform 2)
/FTId=VSP 007172.
                                                                                                                                                                                                                                                                                                                                                                                                                        Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Interacts with the NAC protein TIP. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRR 1.
LRR 2.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=1;
IsoId=Q8W4J9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homologs;
WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000767; Disease resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF089710; AAC83165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF089711; AAC78631.1; -. EMBL; AAF24474; AAF36987.1; -. EMBL; AAB025638; BAA97456.1; -. EMBL; AY065514; AAM132592.1; -. EMBL; AX118862; BAC43449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00560; LRR; 2.
Pfam; PF00931; NB-ARC;
                                                                                                                                                                                                                                                                                                                                    defense response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      842
192
294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP BIND
VARSPLIC
```

|::|| | || 883 EKLVPGGEDY 892

```
ö
                                    | Section | Sect
 (in cv. Landsberg erecta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEAK -> FLAG (in cv. Landsberg erecta).
NLRVDT -> DLSVHB (in cv. Di-17).
RVDTB -> SVNNK (in cv. Landsberg erecta).
Q -> E (in cv. Di-17).
YL -> HI (in cv. Di-17).
Missing (in cv. Di-17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erecta).

T -> I (in cv. Di-17).

S -> R (in cv. Di-17).

S -> R (in cv. Di-17).

H -> Q (in cv. Di-17).

I -> L (in cv. Landsberg erecta).

KNKT -> RNNA (in cv. Di-17).

K -> N (in cv. Landsberg erecta).

PRFEEDYW -> WDEDFG (in cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRF -> SRFK (in cv. Di-17).

Y -> F (in cv. Di-17).

S -> Y (in cv. Landsberg erecta).

C -> S (in cv. Di-17 and cv. Landsberg erecta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> N (in cv. Landsberg erecta).
                                                                                                                                                                                                                                                                                        -> S (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                      Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                 -> R (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                      DSEESTYSLEY -> YSKISAYDLFN (in cv. Landsberg erecta).
EISTYS -> KITTQE (in cv. Di-17).
A -> V (in cv. Landsberg erecta).
B -> Q (in cv. Landsberg erecta).
DNYLSWQ -> NKYLKVH (in cv. Di-17).
NN -> SH (in cv. Landsberg erecta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> S (in cv. Di-17 and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M -> K (in cv. Landsberg erecta).
YLY -> FLF (in cv. Landsberg erecta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 -> FR (in cv. Di-17).
-> H (in cv. Landsberg erecta)
-> Q (in cv. Di-17).
-> G (in cv. Di-17).
IDGQL -> VDEQI (in cv. Landsberg
G -> E (in cv. Di-17).
SGK -> RGE (in cv. Di-17 and cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                 erecta). N -> F (in cv. Di-17 and
                                                                                                                                                                                                                                                                                                       erecta).
W -> C (in cv. D
erecta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1
Pred. No. 53;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               erecta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erecta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erecta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                         481
486
489
514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543
550
549
565
   31
29
87
                                                                                                                                                                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                      399
                                                                                                                                                                                                                                                                                                                                                   426
                                                                                                                                                                                                                                                                                                                                                                                429
                                                                                                                                                                                                                                                                                                                                                                                                              446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4480
4880
4880
4885
                                                         630
632
653
653
656
676
692
697
                                                                                                                                                                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                      399
                                                                                                                                                                                                                                                                                                                                                   426
                                                                                                                                                                                                                                                                                                                                                                                429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
VARIANT
VARIANT
VARIANT
                                                                                                                              VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
VARIANT
VARIANT
                                                                     VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                         VARIANT
```

```
SEQUENCE FROM N.A., AND FUNCTION.
STRAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAINE-SYSTAI
                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Rukaryota, Viridiphantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1; Length 910;
Pred. No. 53;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding, Repeat, Leucine-rich repeat (45 LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 199 ATP (POTENTIAL).
910 AA; 105263 MW; 5B1E9F65A19A12EE CRC64;
                                        15-5RP-2003 (Rel. 42, Created)
15-5RP-2003 (Rel. 42, Last sequence update)
15-5RP-2003 (Rel. 42, Last annotation update)
Disease resistance protein RPH8A (RPP8 homolog A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
  910 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRR 1.
LRR 2.
ATP (PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NB-ARC
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein MJ0939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein MJ09
MJ0939.
Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::|| | ||
885 EKLVPGGEDY 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   625
869
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 BEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                       NCBI TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
602
844
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homologs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y939 METJA
ID Y939 METJA
AC Q58349;
RP8H ARATH
P59584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERPRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
```

```
OC Archaes, Buryarchaeota; Methanococci; Methanococcales;
OC Archaes, Buryarchaeota; Methanocaldococcus.
OC NUCEL TAXID=2199;
OC STRAIN=2419.
OC STRAIN=2419.
OC STRAIN=2419.
OC STRAIN=341.
OC STRAIN—341.
OC STRAIN—34
```

Search completed: December 22, 2003, 17:42:27 Job time : 5.6 secs

1 EEVVPXGMDYS 11 | | :: | | :: | 141 EEIIENGMEHS 151

ઠે

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                      OM protein - protein search, using sw model
```

December 22, 2003, 17:27:26 ; Search time 25.2 Seconds (without alignments) 112.642 Million cell updates/sec US-09-909-164-13 54 1 EEVVPXGMDYS 11 Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 23:* Database :

sp_virus:*
sp_vertebrate:*
sp_unclassaffied:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp archea:*

sp_bacteria:*

sp_fungl:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_organelle:*

sp_bhage:*

sp_phage:*

sp_phage:*

sp_rodent:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | Q12479 saccharomyc | Q8esv7 oceanobacil | 030260 archaeoglob | Q8dih0 synechococc | O22081 citrus unsh | O22096 citrus unsh | Q8w568 arabidopsis | 09c9t7 arabidopsis | P93782 saccharum o | Q9sn30 arabidopsis | Q43010 oryza sativ | Q88064 oryza sativ | O9qq04 eriocheir s | O8xpa8 clostridium | O52367 rhizobium t | O8k143 rhizobium e |
|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ID | Q12479 | Q8ESV7 | 030260 | Овртно | 022081 | 022096 | Q8W568 | Q9C9T7 | P93782 | 08N30 | 043010 | 088064 | Q9GQ04 | QBXPAB | 052367 | 08KL43 |
| DB | m | 16 | 17 | 16 | 10 | 10 | 10 | 2 | 10 | 10 | 2 | 2 | 'n | 16 | ~ | ~ |
| f Query Match Length DB | 156 | 319 | 363 | 1044 | 341 | 348 | 452 | 460 | 1047 | 1083 | 1084 | 1100 | 219 | 253 | 298 | 368 |
| Query Match | 74.1 | 70.4 | 70.4 | 70.4 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 64.8 | 64.8 | 64.8 | 64.8 |
| Score | 40 | 38 | 38 | 38 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 35 | 35 | 35 | 35 |
| Result No. | 7 | ~ | ო | 4 | ß | 9 | 7 | 60 | o | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
| it. | | ` | \ | | | | | | | | | | | | | |

| Q9xvk4 caenorhabdi O9a382 caulobacter | O9vfi3 aeropyrum p | w | Q8xzl5 ralstonia s | Q946j7 andrographi | Q95p46 carcinus ma | Q9u6a3 callinectes | 017704 caenorhabdi | O52673 escherichia | | 027146 methanobact | Q98k29 rhizobium l | Q8tbj7 homo sapien | Q9vsy8 drosophila | Q8r915 thermoanaer | Q8e519 streptococc | Q8dzw9 streptococc | Q8gp33 lactobacill | Q8u7j0 agrobacteri | Q9yet8 aeropyrum p | 029920 archaeoglob | 029451 archaeoglob | Q98fx1 rhizobium l | Q8tff4 trichoderma | Q8r8z2 thermoanaer | | | Q8g3j2 bifidobacte |
|--|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|
| Q9XVK4 09A3B2 | O9YPI3 | 052680 | QBXZLS | 0946J7 | Q95P46 | Q9U6A3 | 017704 | 052673 | 052666 | 027146 | Q98K29 | Q8TBJ7. | Q9VSY8 | QBR9L5 | Q8E5L9 | Q8DZW9 | Q8GP33 | Q8U7J0 | Q9YET8 | 029920 | 029451 | Q98FX1 | Q8TPF4 | QBRBZ2 | Q9CIN1 | Q9JZP8 | Q8G3J2 |
| 16 | 11 | N | 16 | ដ | S | S | ហ | ~ | ~ | 11 | 16 | 4 | s | 16 | 16 | 16 | ~ | 16 | 11 | 11 | 11 | 19 | m | 16 | 16 | 16 | 16 |
| 425 | 440 | 511 | 517 | 595 | 745 | 1031 | 1150 | 1410 | 1420 | 1474 | 1828 | 748 | 143 | 215 | 222 | 222 | 284 | 290 | 296 | 357 | 366 | 387 | 543 | 558 | 265 | 587 | 671 |
| 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 63.9 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 | 63.0 |
| 35 | 32 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 32 | 34.5 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 |
| 17 | 19 | 50 | 21 | 55 | 23 | 24 | 25 | 56 | 27 | 28 | 53 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

RESULT 1

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
SEQUENCE 1044 A
                                                                       Venter J.C.,
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                    Q8DIH0
Q8DIH0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    022081
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                              RESULT 4
                                                                                                                                                                                                                                                                                                                          Q8DIH0
                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    გ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                     ઠે
                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=HTBBA1 / DSM 14371 / JCM 11309;
STRAIN=HTBBA1 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Blosci. Biotechnol. Blochem. 58:391-395 (1994).

EMBL; Z74920; CAA99201.1; -.

EMBL; Z74920; CAA69762.1; -.

SGD; S0005539; YGR013W.

SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 16; Length 319;
Pred. No. 14;
                                                                                                        74.1%; Score 40; DB 3; Length 156; 77.8%; Pred. No. 2.3; 17.8%; Pred. 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 30:3927-3935(2002).
EMBL, AP004594; BAC12465.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 319 AA; 35617 MW; 3BDAB4BF13E79E37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaeoglobus fulgidus.
Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Oceanobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 AA
                                                                                                                                                                                                                                          319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                 Hypothetical conserved protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein AF2411 AF2411.
                                                                                                                     Local Similarity 77.8
les 7; Conservative
                                                                                                                                                                                                                                                                                                                        Oceanobacillus iheyensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::|| |:||
BOLVPHGIDY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 REVVPXGMDY 10
                                                                                                                                                         2 EVVPXGMDY 10
                                                                                                                                                                     ||:| ||||
50 EVMPLGMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189
                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            030260;
                                                                                                                                                                                                                                                     08ESV7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 030260
                                                                                                                                                                                                                                          OBESV7
                                                                                                                                                                                                                                                                                                               OB0509
                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                RESULT 2
Q8ESV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     030260
   SORBERTA
                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Pujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sucrose-phosphate synthase (Fragment).
CITSPS2.
Citrus unshiu (Satsuma orange).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BP-1;
MREDLINE=2225144; PubMed=12240834;
Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Makamura Y., Kaneko T., Sato S., Ikeuchi M., Kishida Y., Kityokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 16; Length 1044;
Pred. No. 53;
2; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.4%; Score 38; DB 17; Length 363; 54.5%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1044 AA; 113205 MW; 00B9C13F0F636D2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                  InterPro; IPR002103; Bac_luciferase.
Pfam; PF00296; bac_luciferase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE7788F4803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1044 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 9:123-130(2002).
EMBL; AP005374; BAC09170.1; -.
                                                                                                                                                                                                                                                                EMBL; AE001109; AAB91255.1; -. TIGR; AF2411; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multidrug efflux transporter.
TLL1618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  022081;
01-JAN-1998 (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.00,
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 54.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||:| |: ||
843 EEVLPNGIGYS 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 ENIVPYGIDFS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 BEVVPXGMDYS 11
```

452 AA.

```
Cheuk R., Chen H., Kim C.J., Koesema B., Meyers M.C., Banh J.,
BOWSer L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Paln C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosida II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
At1g73750/F25F22_17.
                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcker J.R.;
"Arabidopsis cDNA clones.";
                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 EEDVPSAMDY 219
           |:| |||:|
234 VIPPGMDFS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 REVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                 08M568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9C9T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                         RESULT 7
Q8W568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9C9T7
                                      셤
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-cv. Miyagawa-Wase; TISSUE=Juice sacs and segment epidermis; Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; "Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; Plant Sci. 140:165-178(199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Juice sacs and segment epidermis;

Komateu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;

"Differential expression of three sucrose-phosphate synthase isoforms
during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";

Plant Sci. 140:169-178(1999).
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=55188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Sapindales, Rutaceae, Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                 STRAIN=cv. Miyagawa-Wase; TISSUB=Juice sacs and segment epidermis; MEDLINE=56439642; PubMed=8842155; Komatsu A., Takanna T.; Komatsu A., Takannokura Y., Omura M., Akihama T.; "Cloning and molecular analysis of CDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Komatsu A., Takanokura Y., Omura M., Akihama T.; "Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%; Score 36; DB 10; Length 341; 66.7%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 36; DB 10; Length 348; 66.7%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 AA; 38136 MW; 61417A69C4560777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 AA; 38556 MW; BEIC21EBA6FF5C5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Juice sacs and segment epidermis;
MEDLINE-96439842; PubMed-8842155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sucrose-phosphate synthase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                  Marc.).";
Mol. Gen. Genet. 252:346-351(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marc.).";
Mol. Gen. Genet. 252:346-351(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citrus unshiu (Satsuma orange).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| |||:|
228 VIPPGMDFS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 022096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      022096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
022096
022096
AC 01-21
DT 01-21
DT 01-21
DT 01-21
DT 01-21
DE CITY
OC BURN
OC CITY
OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
```

셤

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Carminci P., Chen H., Cheuk R., Shinn P., Banh J., Bowser L.,
Carminci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sarkrai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 36; DB 10; Length 452; 70.0%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                        EMBL; AY113044; AAM47352.1; -.
InterPro; IPR002471; Prol_endopep_ser.
InterPro; IPR00379; Ser_estre site.
PROSITE; PS00708; PRO SNDOPEP_SER; 1.
SEQUENCE 452 AA; 49682 MW; A159955B21742C4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 50.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
```

3 VVPXGMDYS 11

```
"Structure and RPLP mapping of a rice sucrose phosphate synthase (SPS) gene that is specifically expressed in the source organ."; plant Sci. 112:207-217(1995).
                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. WILPHY G., Ridley P., Hudson S., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 36; DB 10; Length 1083; 66.7%; Pred. No. 1.5e+02; ive 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. japonica;
Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
Fujimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001557; L.LDH.
Pfam; PF00534; Glycos_transf_1; 1.
PR051TF; PS00064; L.LDH; 1.
SEQUENCE 1084 AA; 119417 MW; 4D0D79AFEDD2F92B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122688 MW; BFC126FCA2137BB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

BU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL049487; CAB39764.1; --

EMBL; AL161516; CAB78135.1; --

EMBL; AL161516; CAB78135.1; --

EMBL; PR001296; GIYCO_trans_1.

Pfam; PP00534; GIYCOs trans_1.

GIYCOSYLtransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                    01-MAR-2003 (TrEMBLrel. 13, Last sequence update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14)
P28M11.40 OR AT4G10120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Sucrose phosphate synthase.
                                                                            PRT; 1083 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1084 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                              Created)
                                                                                                                         (TrEMBLrel. 13, (TrEMBLrel. 13,
                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAK-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D45890; BAA08304.1;
Gramene; Q43010; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:| |||:|
483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              043010
                                                                          098N30
                     RESULT 10
Q9SN30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         043010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                  Theologis A., Ecker J.R., Palmer.J., Federspiel N.A., Kaul S.,
Myite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
A Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
A Chung M.K., Conn L., Conway A.B., Conway A.R., Feng J.-D., Fong B., Fujii C.Y.,
A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
A Kim C.J., Koo H.L., Xremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Liee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin K., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziall A.,
A Miltecher J., Miranda M., Nguyen M., Neoney T., Rowley D.,
Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Wu D., Yu G., Praser C.M., Venter J.C., Davis R.W.;
"Lettback T., Van Aken S., Vaysbers M., Wootskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaycotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaycotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaycotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaycotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaycotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaysotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaysotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaysotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaysotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaysotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaysotskaia V.S., Walker M.,
"Lettback T., Van Aken S., Vaysbers M., Vaysotskaia V.S., Walker M., Valler J.C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiharto B., Sakakibara H., Sugiyama T.;
"Differential Expression of Two Genes for Sucrose-Phosphate Synthase
"Differential Expression of Two Genes for Sucrose-Phosphate Synthase
of Gene Expression.",
Submitted (FEBL1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AB001337; BA419241.1;
InterPro; IPR001396; Glyco_trans 1.
Pfam, PR00534; Glycos transf 1; 1.
All 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Saccharum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 36; DB 10; Length 1047; 66.7%; Pred. No. 1.4e+02; tive 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 36; DB 10; Length 460; 70.0%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1047 AA; 116379 MW; DOEDB34961E1D83D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 AA; 50564 MW; E94B27B5C4B249EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Sucrose-phosphate synthase (EC 2.4.1.14) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1047 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000).

EMBL, AC012679; AAG52073.1; -.

InterPro; IPR0012471; Prol_endope_ger.

InterPro; IPR00179; Ser_estre site.

PROSITE; PS00708; PRO_ENDOPEP_SER; 1.

Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharum officinarum (Sugarcane)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.70,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 REDVPSAMDY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 VIPPGMDFS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P93782
```

δ

RESULT 9
193782
100 193782
101 193782
102 193782
103 104-M
105 104

ઠે

ö

Gaps

ô

3

```
Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||::| :||
108 BEIIPDDVDY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGMDY 10
                                                                                                                                                                             107 VPQGLDYS 114
                                                                                                                       4 VPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BTRAIN=13 / Type A;
PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=CFN299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XYLB1.
Rhizobium tropici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY
                                                                                                                                                                                                                                                                                                                                 Q8XPA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      052367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
052367
                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                          SO WE READ TO THE SO OCCORNERS OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                             윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative sucross-phosphate synthase.
P0678F11.14.
P072a sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=G111;
Weihrauch D., Towle D.W.;
Walthrauch D., Towle D.W.;
WaltH-Wackhanger and Na+/K+/2Cl- -cotransporter are expressed in g118 of the euryhaline Chinese crab Briocheir sinensis.";
Comp. Biochem. Physiol. 126:8158-S158 (2000).
EMBL; AF301160; AAG3938.1; -.
NON TER 19 219
NON TER 219 219
SEQÜENCE 219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;
                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                         Score 36; DB 10; Length 1084;
Pred. No. 1.5e+02;
2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 36; DB 10; Length 1100; 66.7%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Na+/K+/201-cotransporter (Fragment).
Eriocheir Sinensis (Chinese mitten crab).
Eviaryota; Metacos, Arthropoda; Crustaces; Malacostraca;
Eumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Grapsoidea; Varunidae; Eriocheir.
NTBI_TAXID=95602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gramene; Q8SO64; -.
InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001557; L_LDH.
Pfam; PF00534; Glycos_transf_1; 1.
PROSITE; PS00064; L_LDH; 1.
SEQUENCE 1100 AA; 121170 MW; 084P4604BA389CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone:P0678F11.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003437; BAB86107.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    PRT; 1100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                            66.7%;
                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| ||:|
469 VIPPGMDFS 477
                                                                                                                                                                                      |:| |||:|
453 VIPPGMDFS 461
                                                                                                                                                 3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VVPXGMDYS 11
                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GQ04
Q9GQ04;
                                                                                                                                                                                                                                                                                                                                                                                             088064;
                                                                                                                                                                                                                                                                                                                                                                 088064
                                                                                                                                                                                                                                                                                                        RESULT 12
Q8S064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                             ACCOCCOS ON THE STATE OF STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenblueth M., Hynes M.F., Martinez-Romero B.;
Submitted (DEC-1997) to the RMBL/GenBank/DDBJ databases.
-I- COFACTOR: ZINC (BY SIMILARITY)
-I- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.8%; Score 35; DB 16; Length 253; 50.0%; Pred. No. 46; 2; Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pRtrCrN299a.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium.
NCBI_TaxID=398;
Score 35, DB 5, Length 219;
Pred. No. 39;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al protein; Complete proteome.
253 AA; 27714 MW; 814DP79D3E0D7486 CRC64;
                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CPE0057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 2), Last annotation update)
Aryl-alcohol dehydrogenase homolog (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002). BMBL; AP003185; BAB79763.1; ...
InterPro; IPR000205; NAD binding.
InterPro; IPR000594; ThiF_domain.
Pfam; PF00899; ThiF; 1.
Hypothetical protein; Complete proteome.
SRQUENCE 253 AA; 27714 MW; 814DF79D3E0D7486
                                                                                                                                                                                                                                                                                                                                         253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 AA.
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF036920; AAC04779.1; -.
InterPro; IPR002328; ADH zinc.
InterPro; IPR002085; Adh zn family.
InterPro; IPR000205; NAD binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
```

```
DR Pfam, PP00107; adh_zinc; 1.

DR PROSTER; PS00059; ADH_ZINC; 1.

KW Metal-binding; Oxidoreductase; Zinc; Plasmid.

FT NON TER 298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 298;

Best Local Similarity 50.0%; Pred. No. 55;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps

Qy 2 EVVPXGMDYS 11

Db 250 EIIPEGADFS 259
```

Search completed: December 22, 2003, 17:51:30 Job time: 26.2667 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

December 22, 2003, 16:41:00 ; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec Run on:

Perfect score:

US-09-909-164-42 52 1 BEVVEXEXHYS/11) Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1107863 seqs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A_Geneseq_19Jun03:* |:- /SIDS1/gcgdata/g Database :

| SIDSI/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1986.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1990.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA2000.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcddata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcddata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcddata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcddata/geneseqfyeneseqp-embl/AA2001.DAT:*
| SIDSI/gcddata/geneseqfyeneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | Description | ¦ `` | Hepatitis C virus | Hepatitis C virus | ່ວ | υ | Hepatitis C virus | Hepatitis C virus | Hepatitis C virus | Hepatitis C virus |
|-----------|--------|-----------------|------|-------------------|-------------------|----------|----------|-------------------|-------------------|-------------------|-------------------|
| SUMMAKIES | | ID | ١4 | ABB80550 | ABB80554 | ABB80555 | ABB80523 | ABB80527 | ABB80531 | ABB80532 | ABB80537 |
| | | DB | 23 | 53 | 23 | 53 | 53 | 23 | 33 | 23 | 53 |
| | | Match Length DB | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 |
| | Query | Match | 94.2 | 94.2 | 94.2 | 94.2 | 92.3 | 92.3 | 92.3 | 92.3 | 92.3 |
| | | Score | 49 | 49 | 49 | 49 | 48 | 48 | 48 | 48 | 48 |
| | Result | So. | - | 7 | m | 4 | 'n | φ | 7 | 80 | 6 |

| Hepatitis C virus Hepatitis C virus | 181 | Hepatitis C virus Hepatitis C virus | 18 C | is C | ن د د | Hepatitio C wime | ່ວ | Ü | U | 0 | Hepatitis C virus | Hepatitis C virus | ပ ပ | ပ မ | و د | Hepatitis C virus | U | Hepatitis C virus | U | ပ် B | 18 C | is C |
|--|---------|--|------------|-------|----------|------------------|---------|-----|-------|-----|-------------------|-------------------|------------|--------|------------|-------------------|----|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----|---------|------|------|
| 11 23 ABB80541 11 23 ABB80558 11 23 ABB80550 | ABB8054 | | 23 ABB8054 | 53 | ABB8055 | 3 5 | ABB8055 | | 53 | | 23 | 53 | 23 ABB8052 | 53 | 23 ABB8052 | 23 ABB8053 | 53 | 23 ABB8053 | 23 ABB8053 | 23 | 23 ABB8053 | 53 | 53 | 53 | 53 | 23 | | 23 | | 53 | 53 |
| 9 9 9 | 76. | | 0 76. | 0 76. | 76. | 20 | 0 76. | 76. | 9 75. | 75. | 75. | 75. | 75 | 9 75 | 75 | 9 75 | 75 | 75 | 75 | 9 75 | 75 | 9 75 | 75 | 75 | 75 | 75 | 75 | 75 | 7 | 75 | 75 |
| PP 110 | £1: | 15 | . 16 | 17 | 80 0 | 20 | 21 | 22 | 23 | 24 | 52 | 56 | 27 | 28 | 53 | 30 | 31 | 32 | 33 | 34 | 32 | 36 | 37 | 38 | 33 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

ABB80546 standard; peptide; 11 AA. ABB80546; RESULT 1 ABB80546

(first entry) 08-OCT-2002

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide. Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26.

Synthetic.

/note= "N-terminal acetyl" Location/Qualifiers Key Modified-site

/note= "Norvalyl carbonyl forming keto-amide linkage with residue ?" Modified-site

11 /note= "C-terminal amide" Modified-site

WO200208251-A2

31-JAN-2002.

19-JUL-2001; 2001WO-US23169.

21-JUL-2000; 2000US-220101P.

```
/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                           ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30
                                                                                                                                                                                                                                                                                       Score 49; DB 23; Length 11; Pred. No. 0.0037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brunck TK;
                          Brunck TK;
                                                                                                                               Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80550 standard; peptide; 11
                                                                                                                                                                                                                                                                                        94.2%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                     10; Conservative
                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGTHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
                          Levy OE,
(CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGXHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-361643/39.
                                                  MPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                        virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                              Novel peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lim-wilby M,
                          Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80550
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
ð
```

Ŕ

```
ö
                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #34
                                                                                                                                                                                                                    ö
                                                                                                                                                                                       Score 49; DB 23; Length 11; Pred. No. 0.0037;
                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŢĶ;
                                                                                                                                                                                                                                                                                                                                           ABB80554 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Norvaly1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 65; 69pp; English
                           Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck
                                                                                                                                                                                       94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                     10, Conservative
                                                                                                                                                                                                                                               1 BEVVPXGXHYS 11
                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levy OE,
                                                                                                                                                                                                                                                                        BEVVPXGSHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-361643/39
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 8
                                                                                                                                                               11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus protease
protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modifled-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                        ABB80554;
 virus
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                           ************
                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                ò
```

ö

Gaps

ö

1; Indels

Mismatches

Length 11;

```
Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                  ABB80523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                        virucide
                                                                                          RESULT
                                                                                                                          ò
                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                ö
 a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                 /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                 Gaps
                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35
                                                                                ö
                                                            Score 49; DB 23; Length 11;
Pred. No. 0.0037;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                    'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                note= "D-form residue"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                        ABB80555 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 65; 69pp; English.
                                                           / Match 94.2%;
Local Similarity 90.9%;
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                 (first entry)
                                                                                                   1 REVVPXGXHYS 11
                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levy OB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                 1 EEVVPXGSHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-361643/39.
                                          11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus protease
                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lim-wilby M,
                                                                                                                                                                                                                  08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2002
                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                              ABB80555;
                                          Sequence
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                    RESULT 4
                                                                                                                                                                ABB80555
  ន្តដ្ឋមូន
                                                                                                   ઠે
                                                                                                                       셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 11;
Score 49; DB 23; Length 11
Pred. No. 0.0037;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 23;
Pred. No. 0.0058;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunck TK;
                                                                                                                                                                                                                                               ABB80523 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.3%;
  94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.3
Best Local Similarity 90.9
Matches 10, Conservative
                                                                                        7
                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EBVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 REVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORV-) CORVAS INT INC
                                                                                                                                    BEVVPXGSHYS
                                                                                        1 REVVPXGXHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200208251-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                        08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
```

virucide

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                         /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #12.
               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 23; Length 11;
Pred. No. 0.0058;
0; Mismatches 1; Indels
                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                           11
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB80532 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.3%;
                                                                                                                                                                                                                                                                                                                                           19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 REVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                          (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BEVVPXGGHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus protease
                                                                                                                                                                                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Modified-site
                                                                                                                             Key
Modifled-site
                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                           31-JAN-2002
                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB80532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80532
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                          /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 23; Length 11;
Pred. No. 0.0058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                          note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                            'note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                             'note= "D-form residue"
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŢĶ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80531 standard; peptide; 11 AA.
                                             ABB80527 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levy OB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BEVVPXGMHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AA;
                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JAN-2002
                                                                                                                08-OCT-2002
                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel per
activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                               ABB80527;
```

ö

Gape

ö

Query Match

Matches

ò 셤 SXXXE

```
21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                     11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                         virus protease
         WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                  Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-2002
                                                                                                                                                                                                                                                                                                        10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2002
                          31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                           ABB80541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virucide.
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                               ABB80541
                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
           /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                             peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 23; Length 11;
Pred. No. 0.0058;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "N-terminal acetyl"
/note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
                                                               /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "D-form residue"
                                              /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                           Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB80537 standard; peptide; 11 AA
                                                                                                                                                                                                                                                  Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                               92.3%;
90.9%;
                                                                                                                      19-JUL-2001; 2001WO-US23169
                                                                                                                                       21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   1 BEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGGHYS 11
                                                                                                                                                                           Levy OE,
                                                                                                                                                         (CORV-) CORVAS INT INC
                                                                                                                                                                                              WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                             11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                  virus protease
                                                                                 WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                           Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-2002
                                                                                                   31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virucide
                                                                                                                                                                                                                       activity
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80537
                                                                                                                                                                                                                Novel
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.3%; Score 48; DB 23; Length 11; 90.9%; Pred. No. 0.0058; 1:ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80541 standard; peptide; 11 AA.
                                                                                                                                                                                                  Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 64; 69pp; English
19-JUL-2001; 2001WO-US23169.
                                                                 21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                  Levy OE,
                                                                                                                                (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEVVPXGQHYS
                                                                                                                                                                                                                                                                WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
```

Ç

ö

Gaps

ö

```
The sequence represents a peptide compound of the invention having the peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
activity useful for treating disorders associated with hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40.
                                                                                                                                                                                                                                                            Score 48; DB 23; Length 11;
Pred. No. 0.0058;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              notes "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80560 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 65; 69pp; English
                                                   Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brunck
                                                                                                                                                                                                                                                          92.3%;
Local Similarity 90.9%;
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levy OE,
                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGXHYS
                                                                                                                                                                                                                                                                                                                                                                      BEWPXGMHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-361643/39
                                                                                                                                                                                                                             11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                    virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80560;
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8X1717X8X8X8X8X8X8X171717177777777
$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                         The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory
                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                       DB 23; Length 11; 0.0058; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB 2
Pred. No. 0.005
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                      Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB80558 standard; peptide; 11 AA.
                                                                                                                                                                                            Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.3%;
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEWPKGQHYS 11
                                                      Lim-wilby M, Levy OB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levy OB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                    (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGXHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-361643/39
                                                                                       WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                             virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virucide
```

RESULT 11 ABB80558

ò 요 Gape

ö

2; Indels

```
"Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #25.
   DB 23; Length 11;
   Score 40; DB :
Pred. No. 0.23
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                              ABB80545 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
   76.9%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2001, 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                            (first entry)
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 81.8
                                                                 1 BEVVPXGXHYS 11
                                                                                               REVVPXGTSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||||||
EEVVPXGTSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 REVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-361643/39.
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim-wilby M,
                                    6
                                                                                                                                                                                                                                             08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                        Synthetic.
 Query Match
Best Local S
Matches
                                                                                                                                                                                                             ABB80545;
                                                                                                                                                                                                                                                                                                                            virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                               셤
                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         윱
                                                                                                                                                                                              ö
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             otide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #24
                                                                                                                                                                                              ö
                                                                                                                                                             Length 11;
                                                                                                                                                               Score 48; DB 23;
Pred. No. 0.0058;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŢĶ;
                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brunck
                                                                                                                                                                                                                                                                                                                                         ABB80544 standard; peptide; 11
                                                                                                                                                             92.3%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                            EEVVPXGXHYS 11
                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Levy OE,
                                                                                                                                                                                                                                                 EEVVPXGMHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-361643/39.
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                               11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2002
```

Synthetic.

virucide

ABB80544;

Sequence

\$8888888888

Matches

g

ò

```
ö
                                                                                                                                                                                                                            pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%; Score 40; DB 23; Length 11; 81.8%; Pred. No. 0.23; 2; Indels tive 0; Mismatches 2; Indels
```

Sequence

Novel

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                   /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory sectivity useful for treating disorders associated with hepatitis C virus protease -
                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 23; Length 11;
Pred. No. 0.23;
0; Mismatches 2; Indels
                                                                                                                                                                                                                       'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brunck TK;
ABB80547 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n 76.9%;
Similarity 81.8%;
9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-2000; 2000US-220101P
                                                        08-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                             WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus protease
                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                          31-JAN-2002.
                                                                                                                                                              Synthetic
                             ABB80547;
```

Search completed: December 22, 2003, 17:41:02 Job time : 33.4667 secs 1 BEVVPXGTDYS 11 a

1 REVVPXGXHYS 11

ઠે

ö

Gapa

us-09-909-164-42.rai

```
Sequence 21444, A Sequence 4794, Ap Sequence 26615, A Sequence 3, Appli Sequence 6771, Ap Sequence 182, App Sequence 182, Appli Sequence 6, Appli Sequence 66, Appli Sequence 56, Appli Sequence 56, Appli Sequence 56, Appli Sequence 56, Appli Sequence 10, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6440, Ap
3, Appli
5, Appli
7, Appli
9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            December 22, 2003, 16:37:03 ; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued Patents AA:*

(Ggn2_6/ptodata/1/iaa/5A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/5B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-21444
US-09-134-001C-4794
US-09-134-001C-4794
US-09-134-001C-4794
US-09-134-001C-4794
US-08-134-001C-4794
US-08-107-512A-6771
US-08-961-083-182
US-09-516-083-182
US-08-961-083-182
US-08-961-083-66
US-08-961-083-66
US-09-961-083-66
US-09-961-083-66
US-09-961-083-56
US-09-961-083-56
US-09-961-083-56
US-09-36-784-56
US-09-36-784-56
US-09-36-784-56
US-09-36-784-56
US-09-961-083-56
US-09-961-083-56
US-09-961-083-56
US-09-468-656A-4
US-09-38-784-1018-3
US-08-530-010-7
US-08-530-010-11
US-08-530-010-11
US-08-530-010-11
US-08-484-1018-3
US-08-484-1018-3
                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                 US-09-909-164-42
52
                                                                                                                                                                                                       1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
No.
```

| 2 01.5 738 2 US-08-404-1018-13 Sequence 9, Appl. 12 61.5 738 3 US-08-714-524D-3 Sequence 3, Appl. 13 61.5 738 3 US-08-714-524D-5 Sequence 5, Appl. 12 61.5 738 3 US-08-714-524D-7 Sequence 7, Appl. 12 61.5 738 3 US-08-714-524D-7 Sequence 7, Appl. 12 61.5 738 3 US-08-714-524D-9 Sequence 9, Appl. 12 61.5 738 3 US-08-714-524D-9 Sequence 9, Appl. 12 61.5 738 3 US-08-714-524D-11 Sequence 11, Appl. 12 61.5 738 3 US-08-714-524D-11 | 4 US-09-252-991A-32960 4 US-09-134-001C-3950 4 US-09-134-001C-3950 4 US-09-328-352-7284 4 US-09-342-647-4 2 US-08-459-146-2 2 US-08-459-146-2 4 US-09-342-647-2 4 US-09-342-647-2 4 US-09-342-647-2 4 US-09-342-647-28 | |
|---|--|--|
| 35 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | | |

```
RESULT 1

US-09-252-991A-21444

; Sequence 21444, Application US/09252991A
; Sequence 21444, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: NUMBER: US/09/252,991A
    TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
    TILL OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
    TILL OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
    TILL OF DATE: 1998-02-18
    PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR PILING DATE: 1998-02-18
; PRIOR PILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; RENOTH: 856
    TYPE: PRT
    CRACHIS SEG ID NOS: 33142
; GROWISM: PRUMBER: US 60/094,190
; TYPE: PRT
    CRACHIS SEG ID NOS: 33142
; GROWISM: PRUMBER: US 60/094,190
; GROWISM: PRUMBER: US 60/094,190
; RIGHTH: 856
; GROWISM: RIGHTH: 856
; GROWISM:
```

 Qy
 1 BRVVPXGXHY 10

 Db
 64 EAVVPGGEHY 73

TRESULT 2
US-09-134-001C-4794

Sequence 4794, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU

TITLE OF INVENTION: USIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR PLICHING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4794

TYPE: PRT

δ g

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 2; Length 126;
Pred. No. 12;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09215096;
Patent No. 6008194
GENERAL INFORMATION
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELEPOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/879,995
FILING DATE:
                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 EQVVPGGGH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 163590
                                                                                                                                                                                                                                                                                                                                          LIBRARY: GenBank
CLONE: 163590
                                                                                                                                                                                                                                                                                                                                                                                         US-08-879-995A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-215-096-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: STATE:
                                                                                                                                              TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                      Sequence 26615, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26615
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                      Query Match
69.2%; Score 36; DB 4; Length 1037;
Best Local Similarity 63.6%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.3%; Score 35; DB 4; Length 277; 63.6%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08879995A
Patent No. 5985606
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STRET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COMPUTRY: USA
COMPUTRY: USA
COMPUTRY: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
HILL OF DATA.
APPLICATION DATA:
HILL OF DATA.
HILL DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
  ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 67.3
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTRODUCT ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: Herewith
                                                                                                                                                                                                     1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 EETVPGGGHTS 58
                                                                                                                                                                                                                                                                                                                      US-09-252-991A-26615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-26615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-879-995A-3
```

ò g

```
3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-536-784-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                              Gaps
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                 65.4%; Score 34; DB 3; Length 126; 66.7%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%; Score 33; DB 4; Length 63; 45.5%; Pred. No. 8.5; tive 3; Mismatches 3; Indels
                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USAL

ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPR: CD/ROM ISO9660
COMPUTER: PC
COMP
                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...63
; SEQUENCE DESCRIPTION: SEQ ID NO: 6771:
US-09-107-532A-6771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6771, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
                                                             Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:: | ||:
BEIMAFGDHYN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EBVVPXGXHYS 11
                                                                                                                                                                                                                                                    28 EQVVPGGGH 36
                                                                                                                                                                                                            1 EEVVPXGXH 9
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-107-532A-6771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
US-09-215-096-3
                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
```

RESULT 7 US-08-961-083-182

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6573082

Requence 182, Application US/09536784

Patent No. 6573082

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TITLE OF INTENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Sequence 182, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: Maryland
COUNTRY: Nockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 3; Length 447; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM:
SOFTWARE: AGCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
FRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BICOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 936,373
REGISTRATION 109-851
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-961-083-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| | ||
178 IVPHGGHY 185
```

```
COMPUTER: HP Vectra 486/33

COMPUTER: WESTING STATEM
MESSISTATION
MESS
```

```
## STRANDEDNESS: single
## MOLECULE TYPE: protein
## MOLECULE TYPE: protein
## SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-09-536-784-56

Query Match

Best Local Similarity 62.5%; Pred. No. 1.46+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0

Qy 3 VVPXGXHX 10

IN | | | | | | |

Db 185 IVPHGDHY 192

Search completed: December 22, 2003, 16:43:44
Job time: 10.1333 secs
```

```
2003, 16:40:14; Search time 20.8667 Seconds (without alignments) 98.451 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/PCT_RBW_PUB.pep:*

3: \cgn2_6/ptodata/2/pubpaa/PCT_RBW_PUB.pep:*

4: \cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

5: \cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: \cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

7: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

10: \cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

11: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: \cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: \cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

15: \cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

15: \cgn2_6/ptodata/2/pubpaa/US10N_PUBCOMB.pep:*

16: \cgn2_6/ptodata/2/pubpaa/US10N_PUBCOMB.pep:*

17: \cgn2_6/ptodata/2/pubpaa/US10N_PUBCOMB.pep:*

18: \cgn2_6/ptodata/2/pubpaa/US10N_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               696363 seqs, 186758610 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                              US-09-909-164-42
52
1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                            December 22,
                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query
No. Score Match Length DB ID

2 34 65.4 715 11 US-09-769-736-24 Sequence 16, Appl 4 55.4 715 11 US-09-252-088-16 Sequence 16, Appl 5 34 65.4 715 11 US-09-252-088-16 Sequence 16, Appl 6 34 65.4 793 11 US-09-769-18 Sequence 15, Appl 6 34 65.4 793 12 US-10-340-792-16 Sequence 15, Appl 6 34 65.4 793 12 US-10-792-16 Sequence 15, Appl 6 34 65.4 793 12 US-10-792-18 Sequence 15, Appl 7 33 63.5 484 11 US-09-769-78-18 Sequence 18, Appl 8 33 63.5 484 11 US-09-769-78-18 Sequence 24, Appl 10 33 63.5 763 9 US-09-769-78-18 Sequence 24, Appl 11 33 63.5 763 9 US-09-765-272-66 Sequence 56, Appl 11 33 63.5 96 9 US-09-765-272-66 Sequence 194, Appl 12 US-09-765-272-66 Sequence 194, Appl 13 63.5 838 11 US-09-884-4655-8 Sequence 7, Appl 14 33 63.5 838 11 US-09-884-4655-8 Sequence 10, Appl 14 33 63.5 838 11 US-09-884-4655-8 Sequence 10, Appl 15 33 63.5 838 11 US-09-884-4655-8 Sequence 10, Appl 15 33 63.5 838 11 US-09-884-4655-8 Sequence 10, Appl 15 33 63.5 838 11 US-09-884-4655-8

RESULT 2 US-09-252-088-16 ; Sequence 16, Application US/09252088 ; Publication No. US20030031682A1

| Sequence 6, Appli Sequence 32486, A Sequence 24, Appl Sequence 164, Appl Sequence 164, Appl Sequence 36, Appl Sequence 38, Appl Sequence 22, Appl Sequence 22, Appl Sequence 131, Appl Sequence 104, Appl Sequence 104, Appl Sequence 104, Appl Sequence 27, Appl Sequence 26, Appl Sequence 27, Appl Sequence 32, Appl | ngth 381; Indels 0; Gaps 0; |
|---|---|
| 11 US-09-884-465A-6 12 US-10-029-386-32486 12 US-10-029-386-32486 13 US-10-108-307-24 14 US-10-108-307-24 15 US-10-116-76-11332 16 US-10-171-404A-36 17 US-09-94-455-164 18 US-10-171-404A-36 18 US-10-171-404A-36 19 US-10-171-29-104 19 US-10-298-638-27 19 US-10-298-638-27 19 US-10-298-638-27 20 US-10-398-638-27 20 US-10-398-638-75 21 US-10-398-638-75 21 US-10-328-638-75 22 US-10-328-638-75 23 US-10-328-638-75 24 US-10-267-74 25 US-10-267-74 25 US-10-122-067-2 25 US-10-122-067-2 26 US-10-122-067-2 27 US-10-122-067-2 28 US-10-122-067-2 28 US-10-122-067-2 | red 769,736 35.5 // 5163 6 8 8 8 No. 98; Le d. No. 98; Le d. No. 98; Alematches 2; |
| 1039 111 153 123 345 122 345 122 345 122 345 122 349 125 11463 125 144 10 144 10 144 10 148 112 148 11 | Technics Richard W remy M Sean B 2089wo 2089wo 2083 02- 203-02- BER: US 99-03-19 212 r. 2.1 r. 2.1 r. 2.1 r. 2.1 75.0%; |
| | APPLICANT: Microbial Technics Limited APPLICANT: Microbial Technics Limited APPLICANT: Microbial Technics Limited APPLICANT: Microbial Technics Limited APPLICANT: Microbial Schaff WF APPLICANT: Meals, Jeremy M APPLICANT: Homiffy, Sean B TITLE OF INVENTION: Proteins FILE REFERENCE: PWC/P21089wo CURRENT FILING DATE: 2003-02-14 PRIOR APPLICATION NUMBER: GB 9816335.5 PRIOR APPLICATION NUMBER: GB 9816335.5 PRIOR APPLICATION NUMBER: GC 0/125163 PRIOR FILING DATE: 1999-03-19 NUMBER OF SEQ ID NOS: 212 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 24 LENGTH: 381 TYPE: PRT ORGANISM: Streptococcus agalactiae GRANISM: Streptococcus agalactiae GrANISM: Streptococcus agalactiae GrANISM: Streptococcus agalactiae GrO9-769-736-24 Query Match 3 VVPXGXHY 10 A 3 VVPXGXHY 10 A 3 VVPXGXHY 10 |
| 16 33 17 32 18 32 19 32 20 32 21 32 22 32 24 32 25 32 26 32 26 31 30 31 31 31 32 31 34 31 36 31 36 31 37 31 38 31 44 31 44 31 45 31 46 31 47 31 48 31 | GEMERAL INFORM APPLICANT: MI APPLICANT: W APPLICANT: W APPLICANT: W TITLE OF INVE FILE REFERENC CURRENT FILING FRIOR APPLICAN FRIOR PILING FRIOR APPLICAN FRIOR FILING FRIOR PILING FRIOR PILING FRIOR PILING FRIOR FILING FRIOR FILING FRIOR PILING FRIOR FILING FRIOR PILING FRIOR FILING FRIOR APPLICAN FRIOR FILING FRIOR APPLICAN FRIOR FILING FRIOR FILING FRIOR |

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.4%; Score 34; DB 11; Length 793; 75.0%; Pred. No. 2.1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15. Application US/10340792
Fublication No. US20030228323A1
GENERAL INFORMATION:
APPLICANT: BRODEN; Bernard R.
APPLICANT: BRODEN; Bernard R.
APPLICANT: BOYER, Martine
APPLICANT: HAMEL; Josee
APPLICANT: HAMEL; Josee
CURRENT HAMEL; Josee
FILE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 3313-9002
CURRENT FILING DATE: 2003-01-13
FRIOR PLING DATE: 2003-01-13
FRIOR PLING DATE: 1999-02-18
FRIOR PLING DATE: 1999-02-18
FRIOR PLING DATE: 1999-02-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN OF: 2003-01-3
SOFTWARE: PATENTIN OF: 2003-
                 APPLICANT: CHARLEBOIS, Isabelle
APPLICANT: HAMEL, Jose
APPLICANT: HAMEL, Jose
APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REPERENCE: 8331-9002
CURRENT PELLING DATE: 1999-02-18
CURRENT PELLING DATE: 1999-02-18
CURRENT PELLING DATE: 1999-02-18
SARLIER FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 65.4%; Score 34; DB 12; Best Local Similarity 75.0%; Pred. No. 2.1e+02; Matches 6; Conservative 0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-769-736-18
; Sequence 18, Application US/09769736
; Publication No. US20030138775A1
; GENERAL INFORMATION:
; APPLICANT: Merobial Technics Limited
; APPLICANT: Wells, Jeremy M
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: group B streptococcus
US-09-252-088-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: group B streptococcus
US-10-340-792-15
APPLICANT: BOYER, Martine APPLICANT: CHARLEBOIS, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 WPHGDHY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 WPHGDHY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 WPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-340-792-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.4%; Score 34; DB 11; Length 715; Best Local Similarity 75.0%; Pred. No. 1.9e+02; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.4%; Score 34; DB 12; Length 715; 75.0%; Pred. No. 1.9e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BRODGUR, Bernard R.
APPLICANT: BRODGUR, Bernard R.
APPLICANT: BOYER, Martine
APPLICANT: BOYER, Martine
APPLICANT: HAMEL, Josee
APPLICANT: HAMEL, Josee
CURRENT PRIJICANT: WARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REPERENCE: 3313-900
CURRENT APPLICATION NUMBER: US/10/340,792
CURRENT FILING DATE: 1999-02-18
PRIOR PLICATION NUMBER: US/60/075,425
PRIOR PLICATION NUMBER: US/60/075,425
PRIOR PLICATION NUMBER: US/60/075,425
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PALENTIN OFF: 2.0
SOFTWARE: PALENTIN OFF: 2.0
SOFTWARE: PALENTIN OFF: 2.0
                        APPLICANT: BRODECK, Bernard R.
APPLICANT: BRODECK, Glment
APPLICANT: BOYER, Martine
APPLICANT: CHARLEBOIS, Isabelle
APPLICANT: CHARLEBOIS, Isabelle
APPLICANT: HAMEL, Jose
APPLICANT: MARTIN, Dones
APPLICANT: MARTIN, Dones
ITILE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REPRENCE: 8131-9002
CURRENT APPLICATION NUMBER: US/60/075,425
EARLIER APPLICATION NUMBER: US/60/075,425
SARLIER PILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN OF: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09252088; Publication No. US20030031682A1; GENERAL INFORMATION:
APPLICANT: BRODEUR, Bernard R.; APPLICANT: RIOUX, Clment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: group B streptococcus
US-09-252-088-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: group B streptococcus US-10-340-792-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 VVPHGDHY 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 WPHGDHY 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WPXGXHY 10
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-10-340-792-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-088-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 16
LENGTH: 715
```

ò 쉽 ö

ð 셤

```
: | | | | | 111 178 1VPHGGHY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-769-744A-24
                                                                                                                 US-09-769-787-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: PE
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYRE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,272 FILING DATE: 22-Jan-2001 CLASSIPICATION: CURNOWN>
PRIOR APPLICATION: CUNCHOWN>
PRIOR APPLICATION NUMBER: 08/961,083 FILING DATE: CUNCHOWN>
APPLICATION NUMBER: 08/961,083 FILING DATE: CUNCHOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders REFERENCE/DOCKET NUMBER: 36,373 REFERENCE/DOCKET NUMBER: 98,340P2 TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHMONE: (2011) 309-8594
                                                                                                                                                                                                                                                                                                                                   Score 34; DB 12; Length 822;
Pred. No. 2.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.5%; Score 33; DB 9; Length 447; Best Local Similarity 62.5%; Pred. No. 1.8e+02; Matches 5; Conservative 1; Mismatches 2; Indels
FILE REFERENCE: PWC/P21089wo
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
FRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: 922
LENGTH: 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 182:
US-09-765-272-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 182, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       ) ORGANISM: Streptococcus agalactiae US-09-769-736-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 VVPHGDHY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-765-272-182
                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
```

3 VVPXGXHY 10

ð

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%; Score 33; DB 11; Length 484; 62.5%; Pred. No. 2e+02; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 12; Length 484;
Pred. No. 2e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Segence 24, Application US/09769744A

Publication No. US20030134407A1

GENERAL INFORMATION:

APPLICANT: Le Pege, Richard WF

APPLICANT: Handlify, Sean B

APPLICANT: Handlify, Sean B

TITLE OF INVENTION: Proteins

FILE REPERRENCE, PM(7921122M)

CURRENT APPLICATION NUMBER: US/09/769,744A

CURRENT FILING DATE: 2001-01-26

PRIOR FILING DATE: 1999-07-27

PRIOR FILING DATE: 1999-07-27

PRIOR PAPLICATION NUMBER: GB 9816336.3

PRIOR FILING DATE: 1999-07-27

PRIOR PAPLICATION NUMBER: US 60/125329

PRIOR FILING DATE: 1999-03-19

NUMBER: OF SEQ ID NOS: 196
                                                         APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TILLS OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129W0
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT APPLICATION NUMBER: GB 9816337.1
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SENGTHA: 484
; Sequence 38, Application US/09769787; Publication No. US20030091577A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Streptococcus pneumoniae US-09-769-787-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptococcus pneumoniae US-09-769-744A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | | | | 202 IVPHGGHY 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 WPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 11; Length 826;
Pred. No. 3.5e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%; Score 33; DB 9; Length 796; 62.5%; Pred. No. 3.4e+02; ive 1; Mismatches 2; Indels
                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: cunknown-
ATTORNEY/AGENT INFORMATION:
NAME: BTOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 56:
BEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 194, Application US/09769787
; Bequence 194, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INPORMATION:
    APPLICANT: Midrobial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
    TITLE OF INVENTION: Proteins
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
    CURRENT APPLICATION NUMBER: US/09/769,787
    CURRENT FILING DATE: 1998-03-27
    PRIOR FILING DATE: 1999-03-19
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 194
                      APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09884465A; Publication No. US20030077293A1; GENERAL INFORMATION: APPLICANT: Shire Biochem, Inc.; APPLICANT: Hamel, Josee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.5
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.5
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| | ||
185 IVPHGDHY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 WPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Str
US-09-769-787-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-765-272-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-884-465A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 56, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                   APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OOFWARIS HE SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/765,272 FILING DATB: 22-Jan-2001 CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/961,083 APPLICATION DATA: APPLICATION DATA: ANTORWAY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.5%; Score 33; DB 9; Length 763; Best Local Similarity 62.5%; Pred. No. 3.2e+02; Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM, MSDOS version 6.2 SOFTWARE: AGCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REPERRICE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-765-272-66
                                              Sequence 66, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                      STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 IVPHGDHY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-765-272-56
                           US-09-765-272-66
```

ઠે 셤

ö

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%; Score 33; DB 11; Length 840; 62.5%; Pred. No. 3.6e+02; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 11; Length 838;
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Coullet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REPERENCE: 055190-0044
CURRENT APPLICATION NUMBER: 105/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LEMOTH: 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Osee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denia
APPLICANT: Charland, Nathalie
APPLICANT: Coullet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denia
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/884,465A CURRENT FILING DATE: 2001-06-20 PRIOR APPLICATION NUMBER: 60/212,683 PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-884-465A-10
. Sequence 10, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-884-465A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09884465A
Publication No. US20030077293A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shire Biochem, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.5
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 IVPHGDHY 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 IVPHGDHY 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-884-465A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

Page

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

December 22, 2003, 17:24:36; Search time 9.06667 Seconds (without alignments) 116.675 Million cell updates/sec Run on:

US-09-909-164-42 52

1 EEVVPXGXHYS 11 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:* Database :

1: pirl: * 2: pir2: * 3: pir2: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

| IES | Description | 101010 CC TCTA 4NO | profesi | division p | dependent | L-shaped tail fibe | V1 protein - tobac | tachykinin B precu | hypothetical prote | | 0 | hypothetical 92.4K | carbamoy1-phosphat | hypothetical prote | trans-regulatory s | conserved hypothet | hypothetical prote | 2-methyl-branched- | hypothetical prote | TSI8.1 protein - A | hypothetical prote | | conserved domain p | hypothetical prote | conserved hypothet | hypothetical prote | histidine Motif-Co | conserved hypothet | hypothetical prote | |
|-----------|----------------|--------------------|---------|------------|-----------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---|
| SUMMARIES | Ω | 702590 | A72207 | E69086 | AF3286 | S36851 | A42452 | A25905 | C75538 | T28717 | A69284 | T46758 | F89892 | E97985 | VKLJSI | D82618 | AE2001 | A48702 | S69046 | G86430 | 838143 | C95136 | B95136 | E98004 | G95115 | C97985 | D98004 | H95115 | D97985 | |
| | OB | | 10 | 1 (4 | ~ | 7 | ~ | ~ | ~ | ~ | ď | N | ~ | N | -1 | N | N | 7 | N | ~ | 7 | N | ~ | N | ~ | ~ | N | 7 | ~ | |
| | Length | 233 | 308 | 360 | 1028 | 1396 | 102 | 126 | 279 | 495 | 534 | 822 | 1057 | 46 | 124 | 156 | 252 | 412 | 460 | 510 | 743 | 802 | 819 | 828 | 839 | 853 | 855 | 1039 | 1039 | |
| • | Query Match | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 65.4 | 65.4 | 65.4 | 65.4 | 65.4 | 65.4 | 65.4 | 63.5 | 63.5 | 63.5 | 63.5 | 63.5 | 63.5 | • | e. | m. | | 63.5 | | | 63.5 | 63.5 | 63.5 | |
| | Score | 35 | 9.0 | 32 | | 35 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | |
| | Regult No. | | 7 | Э. | 4 | Ŋ | 9 | 7 | 6 0 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 6 |

| hypothetical prote | prohibitin 2 [impo | GMP synthetase, su | hypothetical prote | fructose-bisphosph | hypothetical prote | probable aspartate | hypothetical prote | probable non-photo | probable bZIP tran | aldehyde dehydroge | DNA mismatch repai | phage transposase | hypothetical prote | macrophage-atimula | ethylene-response |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|
| 857810 | C86169 | H69194 | AF3211 | 847540 | T17267 | G69119 | T24111 | G96568 | G84598 | AI3544 | A69663 | A91247 | 861239 | JC5061 | A48246 |
| 7 | N | ~ | 7 | ~ | ~ | ~ | ~ | ~ | ~ | ~ | N | ~ | ~ | - | 7 |
| 225 | 286 | 311 | 322 | 364 | 369 | 374 | 425 | 454 | 519 | 536 | 627 | 969 | 701 | 716 | 738 |
| 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 | 61.5 |
| 32 | 35 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 35 | 32 | 32 | 32 | 32 | 32 | 32 |
| 30 | 31. | 32 | 33 | 34 | 38 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

| _ | |
|--------|--------|
| RESULT | T02590 |

DNA 2010
CLACCAGE
CLA

Gaps ö h Similarity 60.0%; Pred. No. 9.8; Similarity 60.0%; Pred. No. 9.8; 6; Conservative 1; Mismatches 3; Indele Best Local Similarity Matches 6; Conserv Query Match

ö

1 EEVVPXGXHY 10

ò 셤

90 QAVVPKGRHY 99

field proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: In-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72207
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hick.
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D

Gaps . 0 Query Match 67.3%; Score 35; DB 2; Length 308; Best Local Similarity 75.0%; Pred. No. 13; Matches 6; Conservative 0; Mismatches 2; Indels 2,

```
A; Molecule type: DNA
A; Readdues: 1-1396 «KAL»
A; Readdues: 1-1396 «KAL»
A; Cross-references: EMBL»
A; Cross-references: EMBL»
A; Cross-references: EMBL»
B; Railman, A.V.; Kryukov, V.M.; Bayev, A.A.
Nucleic Acids Res. 16, 6230, 1988
A; Title: The nucleotide sequence of bacteriophage T5 DNA at the region between early a: A; Title: The nucleotide sequence of bacteriophage T5 DNA at the region between early a: A; Reference number: S01982; MUID: 88289370; PMID: 3267228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yel
A;Reference number: A42452; MUID:92188538; PMID:1546458
R;Kaliman, A.V.; Kulshin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NiAlternate processions (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: A25905
R;Kotani, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7074-7078, 1986
A;Title: Structure and gene organization of bovine neuromedin K precursor.
A;Reference number: A25905; MUID:86313713; PMID:3462746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Realdues: 1-126 < KOT>
A; Cross-references: GB: M41351; NID:g163587; PIDN: AAA30723.1; PID:g163590
C; Superfamily: neurokinin B precursor
F;1-26/Domain: signal sequence #status predicted < SIG>
F;27-126/Product: protachykinin B #status predicted < MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: A42452
A,Molecule type: DNA
A,Residues: 1-102
A,Residues: 1-102 (AOR>
A,Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                  FBBS Lett. 366, 46-48, 1995
A;Title: The nucleotide sequence of the bacteriophage T5 ltf gene.
A;Reference number: 865934; MUID:95309401; PMID:7789514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.4%; Score 34; DB 2; Length 102; 60.0%; Pred. No. 6.5; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 68;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%; Score 35; 50.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Gene: ltf
C, Keywords: late protein; tail fiber
                                                                                                                                                                                                                                                                                                                                 A)Accession: 801984
A)&Catesion: 801984
A)&Catesion: Examilation not shown
A)Molecule type: DNA
A),Residues: 934-985, A', 987-1396 <K
A;Cross-references: EMBL:X07559
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.00,
S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tachykinin B precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1360 KTIPAGDHYS 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                    A, Accession: S65934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           È
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                              C. Species: Methanobacterium thermoautotrophicum (strain Delta H)
C. Species: Methanobacterium thermoautotrophicum
C. Species: Methanobacterium thermoautotrophicum
C. Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C. Accession: B69086
C. Accession: B69086
C. Accession: B69086
C. Accession: B69086
K.; Mano, D.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wieczbowski, J.; Gibson, R.; Jiwani, N.; Xi, Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A. Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A. A. Accession: B69086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: AF3286
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Golteman, B.; Selvov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE000923; GB:AE000666; NID:92622766; PIDN:AAB86115.1; PID:9262277
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-dependent DNA helicase BMEI0275 [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-108 «XUR»
A,Cross-references: GB:AE008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
A,Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-360 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-shaped tail fiber protein - phage TS
N'Alternate names: ltf protein
C;Species: phage TS
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: S65934; S01984; $36851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 2
Pred. No. 49;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB :
Pred. No. 16;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: cell division protein MJ0174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.3
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |::|| | |::
98 EDLVPMGSHHT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 BEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |::|| | ||
EKIVPPGARYS
                                             WPSGIHY 48
VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: AF3286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Gene: BMEI0275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: MTH1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
ò
```

ന

```
Coenzyme F420-quinone oxidoreductase (EC 1.6.5.-) 56K chain - Archaeoglobus fulgidus Cispecies Archaeoglobus fulgidus C; Species Archaeoglobus fulgidus C; Species Archaeoglobus fulgidus C; Species Archaeoglobus fulgidus C; Species OS-Dac-1997 #sequence_revision OS-Dec-1997 #text_change 19-may-2000 C; Accession, A69284; 845665.
C; Accession, A69284; 845665.
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dode S; Richerk, A.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dode J; Atuthors Utterback, T.; Octton, M.D.; Spriggs, T.; Artiach, P.; McDonald, L. Nature 390, 364-370, 1997 Penter, J.C.
A; Authors Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archs A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Resenders: 1-534 *KLBs
A; Resenders: 1-534 *KLBs
A; Robers and Seganders: A69250; MUID:98133340; FMID:92689409; PIDN:AAB90959.1; PID:92650; R; Runor, J.; Linder, D.; Stetter, K.O.; Thauer, R.K.
Bur. J. Blochem. 23; 503-511, 1994
A; Title: F(420)H(2): quinone oxidoreductase from Archaeoglobus fulgidus. Characterizat A; Reference number: 845665; MUID:94333340; PMID:8055920
A; Residues: 2, X'.4, X', 4-7, X', 9-10, XX', 13-14 *KUN>
A; Notecule type: Drotein
A; Residues: 2, X'.4, X', 4-7, X', 9-10, XX', 13-14 *KUN>
A; Notecule type: Drotein
A; Residues: 2, X'.4, X', 4-7, X', 5-10, XX', 13-14 *KUN>
A; Notecule type: Drotein
A; Residues: Could not distinguish between glutamate and cysteine for residues C; Superfamily: glutamate synthase small chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cipecies: Streptococcus agalactice
Cipate: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
Cipate: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
Cipate: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
Righellarberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Lu Infect. Immun. 67, 871-878, 1999
A.7Title: Lmb, a protein with similarities to the Lral adhesin family, mediates attachm A.7Title: Lmb, a protein with similarities to the Lral adhesin family, mediates attachm A.7Eeference number: Z24091; MUID:99115568; PMID:9916102
A.8Eeference number: Z24091; MUID:99115568; PMID:9916102
A.8Eefiques: 1-822 csps.
A.7Eesidues: 1-822 csps.
A.7Eesidues: 1-822 csps.
A.7Eesidues: 1-822 csps.
A.7Eeptococcus agalactiae hypothetical 92.4K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N3 C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: E89892 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.4%; Score 34; DB 2; Length 534; 45.5%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 34; DB 2; Length 822; larity 75.0%; Pred. No. 62; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical 92.4K protein - Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 DKVPPHGSHYT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 BEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 VVPHGDHY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
tes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein - Deinococcus radiodurans (strain R1)
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
CiAccession: C75538
Riwhite, O.; Risen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma.; Salth, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
ArTitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
ArEference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75538
A;Accession: Preliminary
A;Accession: Preliminary
A;Restidues: 1-279 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
A;Experimental source: strain R1
C;Genetics:
                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AF022972; PIDN:AAC48234.1; GSPDB:GN00023; CESP:F10D2.3
A;Experimental source: strain Bristol N2; clone F10D2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Caenorhabditis alegaments are responsed to the control of the control 
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR0271
                                       65.4%; Score 34; DB 2; Length 126; 66.7%; Pred. No. 8.2; Arive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.4%; Score 34; DB 2; Length 495; 50.0%; Pred. No. 36; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 2; Length 279;
Pred. No. 19;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 5
A;Introns: 37/2; 90/1; 113/1; 183/3; 356/3; 380/3; 428/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F10D2.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.4%;
Query Match
Best Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 ENIVPTGKHH 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGXHY 10
                                                                                                                                                                                                                                                                               28 EQVVPGGGH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 VPLGRHYS 107
                                                                                                                                                                                                             1 EEVVPXGXH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Gene: CESP: F10D2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
A69284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ö

Gaps

ö

ö

Gapa

ò

Gaps

ö

Length 124 3; Indels

```
Ajaccession: D82618
Ajstetus: preliminary
Ajmolecule type: DNA
Ajendecule type: DNA
Ajmolecule type: DNA
Ajresidues: 1.156 <SIM>
Ajresidues: 1.156 <SIM>
Ajresidues: DNA
Ajvarenga, R.;
Briones, M.R.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, Submitted to GenBank, June 2000
Ajauthors: Perreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fro
J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.B.; Lai
Cando, M.A.; Madelra, A.M. B.N.; Mateina, M.R.; Menck, C.P.M.; Marques, M.V.; Martins, Ajauthors: Martins, B.M.F.; Mateina, M.C.; de Oliveira, R.C.; Palmieri, D
ROGitiques, V.; Rosa, A.J.; de N.; de Rosa Jr., V.B.; de Sal, R.G.; Santelli, R.V.; Sawas
Ajauthors: Assiva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., Walliada, H.; Vanlada, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
Ajarthors: All Allada, M.C.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
Ajarthors: Allada, A.C.R.; da Silva, W.A.; Verjovski-Almeida, S.; Vettore, A.L.;
Ajarthors: Allada, A.C.R.; da Silva, V. Verjovski-Almeida, S.; Vettore, A.L.;
Ajarthors: Allada, A.C.R.; da Silva, V. Verjovski-Almeida, S.; Vettore, A.L.;
Allada, M.D. Allada, A.C.R.; da Silva, V. Verjovski-Almeida, S.; Vettore, A.L.;
Allada, M.D. Allada, A.C.R.; da Silva, V. Verjovski-Almeida, S.; Vettore, A.L.;
Allada, M.D. Allada, A.C.R.; da Silva, V. Verjovski-Almeida, S.; Vettore, A.L.;
Allada, M.D. Allada, A.C.R.; da Silva, V. Verjovski-Almeida, S.; Vettore, A.L.;
Allada, M.D. Allada, A.C.R.; da Silva, V. Verjovski-Almeida, S.; Vettore, A.L.;
Allada, M.D. Allada, A.C.R.; da Silva, V. Verjovski-Almeida, S.; Vettore, A.L.;
Allada, M.D. Allada, A.C.R.; da Silva, V. Verjovski-Almeida, S.; Vettore, S. Vettore, S. Vettore, S. Vettore, S. Vettore, S. Vettore, S. Vettore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: DB2618
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogan Xylella fastidiosa.
A;Note: for a complete list of authors see reference number A59328 below
                   C;Superfamily: AIDS trans-regulatory splicing protein C;Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
                                                                                                                                                                                               Score 33; DB 1;
Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 33; DB 55.6%; Pred. No. 17; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: December 22, 2003, 17:44:59 Job time : 10.0667 secs
                                                                                                                                                                                                            63.5%;
                                                                                                                                                                                         Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 ETVPAGGNYS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 ERILPOGVH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BEVVPXGXH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: XF1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Genetica:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trans-regulatory splicing protein - simian immunodeficiency virus SIVCpz
N.Alternate names: anti-repression trans-activator; art protein; rev protein; trs protein
C;Species: simian immunodeficiency virus SIVCpz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S09988
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Asture 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: S09988; MUD:90259077; PMID:2188136
                                                                                                                                                                                                                                                                                                                         A/Status: preliminary
A/Molecule type: DNA
A/Molecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein spr0909 [imported] - Streptococcus pneumoniae (strain R6) (Species: Streptococcus pneumoniae (Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 #sequence_revision 23-Oct-2001 #sequence_revision 23-Oct-2001 #sequence_revision 23-Oct-2001 #sequence_revision 23-Oct-2001 #sequence_revision 33-Oct-2001 #sequence_revision 2001 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-46 «KUR»
A;Cross-references: GB:AE007317; PIDN:AAK99713.1; PID:g15458516; GSPDB:GN00174
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Titles: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: P89892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36405.1; PID:9763085 C;Genetics: A;Gene: rev; trs; art
A;Gene: rev; trs; art
A;Introns: 27/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-124 <HUB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 2; Length 46;
Pred. No. 4.5;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 2;
Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 IVPHGGHY 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: spr0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

ö

Gaps ö

DB 2; Length 156;

```
ovis aries
drosophila
bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cryphonectr
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q87qx9 vibrio para
Q8rg86 fusobacteri
P13390 bacteriopha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteriopha
tobacco yel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         staphylococ
chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               saccharomyc
buchnera ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       saccharomyc
methanobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brassica ol
arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caenorhabdi
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rattus norv
vibrio chol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yarrowia li
haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vibrio para
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 schizosacch
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             staphylococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oryctolague
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    salmonella
                                                                December 22, 2003, 16:43:51; Search time 4.6 Seconds (without alignments) 112.455 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8x8j4
P21151
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                              127863 segs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AROA VIBPA
AROA VIBPA
VLIF BPTS
Y11K TYDVA
TROK BOVIN
CARB STAAM
CARB STAAM
REV SIVCZ
UMBI YBAST
UMBI YBAST
WALB BUCBP
YK47 YBAST
GAAB METTH
                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPB_SHEEP
SHOW_DROME
MUTL BACSU
ETRI_BRACI
ETRI_ARATH
CRNC MOUSE
YOS6_CAEEL
YOS6_CAEEL
YOS6_CAEEL
WSRA_VIBCH
WSRA_VIBCH
WRRA_VIBCH
THIK ECOLI
THIK ECOLI
THIK SALIY
                                             - protein search, using sw model
                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
                                                                                                             US-09-909-164-42
52
1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                           Swimmer 41:*
                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
                                                                                                                       Perfect score:
                                                                                                                                                          Scoring table:
                                            OM protein
                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                      Sequence:
                                                                    е
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               33100834654321098765432
33310987654321098765432
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                      056075 p genome po
P08831 bos taurus
P79161 capra hircu
Q28579 ovis aries
Q9uhf0 homo sapien
P22917 bacteriopha
Q57654 methanococc
Q0068 citrus tris
Q91c13 helicobacte
P56006 helicobacte
                 homo sapien
                                                                                                                                                                                                                                  STRAINER FROM N.A.

STRAINERING 2210633 / Serotype O3:K6;

MEDLINE-22508454; PubMed=12620739;

MEDLINE-22508454; PubMed=12620739;

Makino K., Oshima K., Kuckawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasuunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 361:743-749 (2003).

-I. CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =

phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.

-I. PATHWAY Aromatic amino acids blosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF 00210; -; 1.

PROSITE; PS00104; EPSP SYNTHASE 1; 1.

PROSITE; PS000895; EPSP—SYNTHASE 2; 1.

Aromatic amino acid biosynthesis; Transferase; Complete proteome.

SEQUENCE 426 AA; 46094 MM; 373D39CC5BAIF70F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 69.2%; Score 36; DB 1; Length 426; Best Local Similarity 60.0%; Pred. No. 5.3; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sixth step.
--- SUBUNIT: Monomer (By similarity).
--- SUBURITIAR IOCATION: Cytoplasmic (Probable).
--- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                              ALIGNMENTS
              A10C HUMAN
POLG PEMVM
IL1A BOVIN
IL1A CAPHI
IL1A SHEEP
TKNK HUMAN
Y16D BPT4
COAT CTV36
SCOA HELPJ
                                                                                                                                                   SCOA HELPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP005076; BAC59283.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 BEWVPXGXHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 EFVIPAGOHY
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
Kaliman A.V
                        METAL
SEQUENCE
                                                                                                                   Query Match
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOT THE PROCESS OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                           윰
                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstanton the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 184:2005-2018(2002).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + possible to the consideration of the construction of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Ponstein M., Xyrpidas N., Overbeek R.;
Genome sequence and analysis of the oral bacterium Pusobacterium
nucleatum strain ATCC 25586.";
                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANIESE I (BY SIMILARITY).
MANGANESE I AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                      Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterales, Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE010554; AAL94625.1; ALT_INIT. HAWAP; MF 01210; -; 1. InterPro; 1PR006275; CarA L glu. InterPro; 1PR005403; CPase L D. InterPro; 1PR005403; CPase L D2. InterPro; 1PR005403; CPase L D3. InterPro; 1PR005401; CPase L D3. InterPro; 1PR005401; CPase L D3. InterPro; 1PR005401; CPase L D3. InterPro; 1PR004362; MGS 11Ke. Pfam; PP02189; CPSase L Chain; 2. Pfam; PP02180; CPSase L Chain; 2. Pfam; PP02180; CPSase L D3; 1. Pfam; PP02142; MGS; 1.
                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         929
1058
546
1058
210
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=76856;
                                                                                                                                                                                                                                             CARB OR FN0422.
                               CARB FUSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
NP_BIND
METAL
METAL
CARB_FUSIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIF...
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
-1- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88289370; PubMed=3267228;
Kaliman A.V., Kryukov V.M., Bayev A.A.;
#The nucleotide sequence of bacteriophage T5 DNA at the region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-55309401; PubMed-7789514;
Kaliman A.V., Kulehin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
Kryukov V.M.;
"The nucleotide sequence of the bacteriophage T5 ltf gene.";
PEBS Lett. 366:46-48(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%; Score 35; DB 1; Length 1396;
50.0%; Pred. No. 29;
iive 2; Mismatches 3; Indels
                                                                                                                               Score 35; DB 1; Length 1058; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        986 986 V -> A (IN REF. 2).
1396 AA; 147989 MW; 18CD2192P65FFFC1 CRC64;
MANGANESE 2 (BY SIMILARITY)
MANGANESE 3 (BY SIMILARITY)
MANGANESE 3 (BY SIMILARITY)
MW; ED7037AF77C1839F CRC64;
                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                           VLTF_BPT5

1D VLTF_BPT5

1D VLTF_BPT5

1D VLTP_BPT5

1D VLTP_BPT5

10-5M-1990 (Rel. 13, Created)

10-7M-1990 (Rel. 13, Last sequence update)

10-7M-2000 (Rel. 39, Last annotation update)

10-7M-2000 (Rel. 39, Last annotation update)

10-8M-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ001191; CAA04591.1; -.
PIR; 865934; S36851.
Late protein.
COMFLICT 986 986 V
SEQUENCE 1396 AA; 147989 MW;
. 300 300
820 820
832 832
1058 AA; 117451 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X69460; CAA49220.1; -.
                                                                                                                                     67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYMANNOSE O ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.3
Best Local Similarity 50.0
Matches 5, Conservative
                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : :| | |||
1360 KTIPAGDHYS 1369
                                                                                                                                                                                                                                                                                |:|| | :||
190 BIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                 2 EVVPXGXHYS 11
                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10726;
```

```
SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bimilarity)
                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARB STAAM
ID CARB STAAM
                                                                                                                                                                                                                                                                                                     MOD RES
SEQUENCE
                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                         Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                           윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86313713; PubMed=3462746; Kotani H., Hoshimaru M., Nawa H., Nakanishi S.; Kotani H., Hoshimaru M., Nawa H., Nakanishi S.; Structure and gene organization of bovine neuromedin K precursor."; Proc. Natl. Acad. Sci. U.S.A. 83:7074-7078(1986).
-!- FUNCTION: TACHYKININS ARE ACTIVE PRETIDES WHICH EXCITE NEURONS, BVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SWOOTH
                                                                                                                                                                MEDLINE=92188538; PubMed=1546458; MEDLINE=92188538; PubMed=1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.; virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.4%; Score 34; DB 1; Length 102; 60.0%; Pred. No. 3.2; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002621; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIE0AF55B67 CRC64;
                                                                                                   Tobacco yellow dwarf virus (strain Australia) (TVDV)
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1988 (Rel. 09, Created)
10-NOV-1988 (Rel. 09, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K).
                                                 Last sequence update)
Last annotation update)
            102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 AA
                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-JUL-1993 (Rel. 27, Last ann
01-CCT-1993 (Rel. 27, Last ann
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                        EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                            NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAC3 OR NKNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKNK BOVIN
P08858;
           Y11K TYDVA
P31619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKNK_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               윱
```

```
the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lancet 357:1225-1240(2001).

-1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

-1- COPACTOR: Binds 3 manganese ions per subunit (By similarity).
-1- PATHWAY: Arginine blosynthesis.
-1- PATHWAY: Arginine blosynthesis.
-1- PATHWAY: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAINEMISO, ATCC 700699, and N315;
MEDLINE-21311952; PubMed=11418146;
MEDLINE-21311952; PubMed=11418146;
MILL, Otta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kanamori M., Mateumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramateu K.;
"Whole genomic sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-PEB-2003 (Rel. 41, Created)
28-PEB-2003 (Rel. 41, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate syntherase large chain (BC 6.3.5.5) (Carbamoyl-phosphate syntherase amonia chain).
CARB OR PYRAB OR SAV1203 OR SA1046.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain Mu50).
Bacteria, Pirmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION (G-96 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003635; Neurokinin.
InterPro; IPR002040; Tachykinin.
Pfam; PP03823; Neurokinin B; 1.
Probom; PD020370; Neurokinin; 1.
PROSTE; PS00267; TACHYKININ; 1.
Tachykinin; Neuropeptide; Cleavage on pair of basic residues; Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.4%; Score 34; DB 1; Length 126; 66.7%; Pred. No. 4; 2; Indels ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446EP433498EC059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEUROKININ B.
                                                                                                                                                                                                                                                                              EMBL; M14349; AAA30723.1; JOINED.
EMBL; M14350; AAA30723.1; JOINED.
PIR; A25905; A25905.
                                                                                                                                                                                                                 EMBL; M14347; AAA30723.1; JOINED EMBL; M14348; AAA30723.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13871 MW;
                                                                                                                                                                                          EMBL; M14351; AAA30723.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
83
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 BOVVPGGGH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
86
99 1
95
126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 BEVVPXGXH
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
NP BIND
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REV SIVCZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255588
  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the between also informatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                       Refam; Froz. Refam; Revolute; MGS; 1.

Refam; PR02142; MGS; 1.

Refam; PR02142; MGS; 1.

Refam; PR02142; PR0099; CPSASE.

Refam; PR031E; PS00866; CPSASE 1; 2.

DR PROSITE; PS00866; CPSASE 1; 2.

DR PROSITE; PS00866; CPSASE 2; 2.

KW Arginine biosynthesis; Pythindine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Camplete proteome.

FT DOMAIN

FT DOMAIN

FT OMAIN

FT OMAIN.

FT OMAIN.

ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-22040717; PubMed=12044378;
MEDLINE-22040717; PubMed=12044378;
Maba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2004 (Rel. 41, Last annotation update)
28-FEB-2005 (Rel. 41, Last annotation update)
phosphate synthetese ammonia chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetese ammonia chain).
CARB OR PYRAB OR MW1086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ATP (POTENTIAL).
32 ATP (POTENTIAL).
34 MANGANESE 1 (BY SIMILARITY).
36 MANGANESE 2 (BY SIMILARITY).
37 MANGANESE 2 (BY SIMILARITY).
38 MANGANESE 3 (BY SIMILARITY).
39 MANGANESE 3 (BY SIMILARITY).
30 MANGANESE 3 (BY SIMILARITY).
31 MANGANESE 3 (BY SIMILARITY).
31 MANGANESE 3 (BY SIMILARITY).
31 MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 1057;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1057 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                              EMBL; AP003361; BAB57365.1; --
EMBL; AP003132; BAB42298.1; --
HSSP; P00968; ICSO.
HAMAP; MF 01210; --; 1.
InterPro; IPR00549; CPase L D2.
InterPro; IPR00549; CPase L D2.
InterPro; IPR00549; CPase L D3.
InterPro; IPR005481; CPase L D3.
Fram; PP02789; CPSase L Chain; 2.
Fram; PP02789; CPSase L D3; 1.
Efam; PP02181; MSS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153
302
284
298
300
832
832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
NP BIND
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P58940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome.

ATP-binding; Manganese; Complete proteome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 41, Last amocation update)
(Anti-repression transactivator protein) (ART/TRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Genome and virulence determinants of high virulence community.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 MANGANESE I (BY SIMILARITY).
98 MANGANESE I AND 2 (BY SIMILARITY).
00 MANGANESE 2 (BY SIMILARITY).
20 MANGANESE 3 (BY SIMILARITY).
32 MANGANESE 3 (BY SIMILARITY).
117185 MW; D8E3B09F9EGFF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1
Pred. No. 36;
1; Mismatches
                                                                                                                                                                                                                                     similarity).
SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0098; CPSASE.
TICRPAMB; TICRO1368; CPSASE11_lrg; 1.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAR, MP 01210; ...;
InterPro; IRR006275; CarA L glu.
InterPro; IRR006275; CarA L glu.
InterPro; IRR005493; CPase L. D2.
InterPro; IRR005480; CPase L. D3.
InterPro; IRR005481; CPase L. D3.
InterPro; IRR005481; CPase L. D3.
InterPro; IRR00486; MGS Ike.
Pfam; PR00289; CPSase L. Chain; 2.
Pfam; PR02786; CPSase L. Chain; 2.
Pfam; PR02786; CPSase L. D3; 1.
Pfam; PR02187; CPSase L. D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP004825; BAB94951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
820
832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 KIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546
929
1057
546
1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1153
302
208
208
300
830
830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (
01-AUG-1990 (
28-FEB-2003 (
REV protein (
REV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REV SIVCZ
P17280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
SEQUENCE
```

```
MOLB BUCBP
Q89A96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIR=S286C / AB972;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

Araujo R., Aparicio A., Barchell B.G. Badcock K., Benes V., Araujo R., Araujo R., Bowman S., Burckner M., Carpenter J., Cherry J.M.,

Achung B., Churcher C.M., Coster F., Davis K., Davis R.W.,

Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterhoeft A.,

Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,

Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,

Homp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis B.J.,

Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Mosetl D.,

Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
                                                        SEQUENCE FROM N.A.
MEDLINE=90259077; PubMed=2188136;
Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                       Nature 345:356-359(1990).
-!- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
-!- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
-!- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED
BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation, AIDS, Phosphorylation, Nuclear protein. SEQUENCE 124 AA; 13701 MW; F5877D1BDF65A7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 33; DB 1; Length 124; 60.0%; Pred. No. 6.5; 3; Indels ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMEI_YEAST STANDARD; PRT; 460 AA. 003010; P87330; CLOUV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Whelsis negative regulator UMEI. UMEI. OR YPLI39C OR LPT7C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000625; REV protein.
Pfam; PF00424; REV; 1.
                                                                                                                                                                                                                                                                                                                                         EMBL; X52154; CAA36405.1; -. PIR; S09988; VKLJSI. HIV; X52154; REV$CPZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 ETVPAGGNYS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE PROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A364A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.;

The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchnera aphidicola (subsp. Baizongia pistaciae).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                          GO; GO: 000564; C: nucleus; IDA.
GO; GO: 0003714; F: transcription co-repressor activity; IDA.
GO; GO: 000020; P: regulation of meiosis; IGI.
InterPro; IPRO01669; WD40.
SNART; SM00320; WH40; 4.
PROSITE; PS00678; WD REPEATS 1; FALSE NEG.
PROSITE; PS50082; WD REPEATS 2; FALSE NEG.
PROSITE; PS50082; WD REPEATS REGION; FALSE NEG.
Transcription; regulation; Meiosis; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 460;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 AA; 51022 MW; AA6F60448B7BCBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-5EP-2003 (Rel. 42, Created)
15-5EP-2003 (Rel. 42, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
Multidary resistance-like ATP-binding protein mdlB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 80 11.
80 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U10280; AAB40937.1; -. EMBL; U43703; AAB68221.1; -. PIR; S69046; S69046. TRANSFAC; T04309; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316
379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 IVPLGLHY 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGD; S0006060; UMB1.
```

POTENTIAL.

```
1 REVVPXGXHYS 11
502 5
539 5
743 AA;
                                                                                                                                                                                       GAAB METTH
           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP BIND
SEQUENCE
  TRANSMEM
                                                Query Match
                                                                                                                                                              RESULT 12
GAAB METTH
                                                                         Matches
                                                                                                                        셤
                                                                                                                                                                                                   ð
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0008654; P:glycerol-3-phosphate O-acyltransferase acti. . .; IDA.
GO; GO:0008654; P:phospholipid biosynthesis; IDA.
InterPro; IRR002123; Acyltransferase.
Pfam; PPO1553; Acyltransferase; 1.
SMART; SM00653; PisC; 1.
Hypothetical protein; Transmembrane.
TRANSMEM 69 85 POTENTIAL.
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
STRAIN=S288C;
van Vliet-Reedijk J.C., Planta R.J.;
Submitted (WAR-1994) to the EMBL/Genbank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCP1-MET1 intergenic region.
YKRO67W.
                                                                                                                                                                                                                                                                                          DB 1; Length 578;
                                                                                                          EMBL; AE014017; AA027134.1; -.
PROSITE; PS00211; ABC TRANSPORTER 1; FALSE NEG.
PROSITE; PS50833; ABC TRANSPORTER 2; 1.
ATP-binding; Transport; Transmembrane; Complete proteome.
TRANSMEM 26 46
                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                  3B84848CE196ADF7 CRC64;
                                                                                                                                                                                                                                        ABC TRANSPORTER. ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                   743 AA.
                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                          Score 33;
Pred. No.
                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                   66827 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z28292; CAA82146.1; -. PIR; S38143; S38143. SGD; S0001775; GPT2.
                                                                                                                                                                                                                                                                                           63.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      550 EIVESGTHYN 559
                                                                                                                                                                                                                                                                                                                                             2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                   578 AA;
                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                  YK47 YEAST
                                                                                                                                                                          TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                     NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         P36148;
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                    YK47_YEAST
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
 ઠે
                                                                                                                                                                                                                                                                                                                                                                    g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Delta H;

WEDLINE-98037514, PubMed=9371463;

WEDLINE-98037514, PubMed=9371463;

MEDLINE-98037514, Doucette-Etamm L.A., Deloughery C., Lee H.-M., Dubois J.,

Aldredge T., Bashizzaebt R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashizzaebt P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Andredge R., Wicare R., Wang Y., Wierzbowski J., Gibson R.,

Andredge T., Bush D., Safer H., Patwell D., Prabhakar S.,

Andredge C.J., Mao J.-I., Nice P., Noelling J., Reeve J.N.;

Bodougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.;

Andredge Genome sequence of Methanobacterium thermoautotrophicum

deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179-1735-7155(1997).

J. Bacteriol. 179-1735-7155(1997).

J. Bacteriol. 179-1735-7155(1997).

J. Bacteriol. 179-1735-7155(1997).

J. BACTERIOL R. AMP + Liglutamate.

H(2)O = AMP + diphosphate + GMP + L.glutamate.

J. SUMINAY: GMP DISYMIHASE SUBNIT (B) (POTENTIAL).

SUBNINIT (A) AND A GNP SYNTHASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (BC 6.3.5.2) (GMP
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea, Buryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PP00958; GMP synt C; 1.
TIGRFAMs; TIGR00884; guaA Cterm; 1.
Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
                                                                                            Score 33; DB 1; Length 743;
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.5%; Score 32; DB 1; Length 308; llarity 63.6%; Pred. No. 27; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 184 GMP-BINDING (BY SIMILARITY).
29 35 ATP (BY SIMILARITY).
308 AA; 34403 MW; P2DCF6ED202CAECI CRC64;
                                                                                                                                                                2; Indels
POTENTIAL.
84B9946E56BB2F15 CRC64;
                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000850; AAB85215.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAWAP; MP_00345; -; 1.
InterPro; IPR001674; GMP_synt_C.
                                  83644 MW;
                                                                                                                       75.0%;
                                                                                               63.5%;
                                                                                                                              Local Similarity 75.0 tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                           294 WPCGLHY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                             3 WPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetase).
GUAAB OR MIH710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacterium
```

573 AA.

PRT;

STANDARD;

```
SUOX DROMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).
ALDOB.
                                                                                                                                                                                                                                                                                                                                                                           "Cloning and characterization of a full-length cDNA coding for ovine aldolase B from fetal mesonephros.";
Biochim. Biophys. Acta 1219:223-227(1994).
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
-!- PATHWAY: Glycolysis; sixth step.
-!- PATHWAY: Glycolysis; sixth step.
-!- SUBUNIT: Homocteramer (By similarity).
-!- MISCELLANBOUS: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, aldolase A in muscle, aldolase B in liver and aldolase C in brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                   Gianquinto L., Pailhoux B.A., Bezard J., Servel N., Kirszenbaum M.,
                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
MCBI_TaxID=9940,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to class I fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 363;
                                                                                              363 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%; Score 32;
62.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P00883; IADO.
InterPro; IPR00741; Aldolase I.
Pfam; PF00274; glycolytic_enzy; 1.
ProDom; P0001128; Aldolase I; 1.
PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                   TISSUE=Mesonephros;
MEDLINE=94368863; PubMed=8086469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z29372; CAA82563.1; -. PIR; S47540; S47540.
216 REVVESGLHES 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 62.5
                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:| | |
189 EVIPDGSH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EVVPXGXH 9
                                                                                                                                                                                                         Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family.
                                                                                             ALFB SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                g
                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

RESULT 14 SUOX_DROME

```
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Babburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Burton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Helt G., Walson C.R., Miklos G.L.G., RA Ballew R.M., Bauu A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Ballew R.M., Baul A., Barman B.P., Bhandari D., Bolbhakov S., Ballew R.M., Bauch J., Bauthar H., Cadeu B., Enchara J., Baytestern P., Brothier P., Burtis R.C., Busman D.A., Buller H., Cadeu B., Center A., Chandra I., Rabenson K.Y., Bence P.W., Buuch J., Butler H., Cadeu B., Center A., Chandra I., Rabenson K., Doug L.E., Downes M., Duller S., Duller S., Marken B., Delcher A., Danike C., Perraz C., Perraz C., Perras C., Perris R.A., Goog F. Gorrell J.H., Gu Z., Galbart M.M., Glasser K., Aloden K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Raris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibegram C., Jalail M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A., Jalail M., Kalush F., Karpen G.H., Mir, J., J., Liang Y., Lin Z., Liang Y., Lin X., Mister B. B., Rodira C.D., Kraft C., Morris J., Mobhrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Rathort K., Nikon K., Nikon W., Stungski M.P., Smith T., Spien H., & Shiner K., Saden H., & Shiner K., Saden H., & Shiner K., Shang H., Wassenbach J., Kang K., Pan S., Pollard J., Wassenbach J., Waster B., Wang Z.-Y., Wassenman D.A., Weinsech G.M., Stung G., Zhon M., Stung G., Zhon M., Stung G., Zhon M., Stung G., Zhon G., Schen H., & Shiner K., Siden-Kiamos I. Simpson M., Stung G., Zhon G., Schen H., & Shiner K., Shander F., Wang G., Zhon M., Stung G., Zhon G., Schen H., & Shine B.C., Zhon F., Wassenman D.A., Weinselber E., Wassenman D.A., Weinselber E., Spradling A.C., Stapler E., Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Berkeley; TISSUB=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.B.;
"A Drosophila full-length CDNA resource.";
"A Drosophila full-length CDNA resource.";
Genome Biol. 3:RESEARCHO080.1-RESEARCHO080.8(2002).
-!- CATALYTIC ACTIVITY: Sulfite + O(2) + H(2)O = sulfate + H(2)O(2).
-!- COFACTOR: Molybdenum (molybdopterin) and one protoheme group (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: Terminal reaction in the oxidative degradation of sulfur-containing amino acids. It uses cytochrome c as an electron
                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-8EP-2003 (Rel. 42, Last annotation update)
Probable sulfite oxidase, mitochondrial precursor (EC 1.8.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Mitochondrial intermembrane space (By
                                                                                                                                                                                Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: WITH CYTOCHROME B5 AND NITRATE REDUCTASE. SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
                                                                                                                                                               Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
                                                                                                                                                                                                                                                                                                                                 STRAIN-Berkeley;
```

```
MEDLINE-98044033; PubMed = 9384377;
 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
 ઠ
                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          Lypaner, reginuojuybe, Cuized.

Typaner, reginuojuybe, Cuized.

R GO; GO:0008758; Cmitcehondrial intermembrane space; NAS.

R GO; GO:0008482; F:sulfite oxidase activity; NAS.

R GO; GO:0008482; F:sulfite oxidase activity; NAS.

R GO; GO:0003163; P:protein catabolism; NAS.

R InterPro; IPR001199; Cyt B5.

R InterPro; IPR0015066; Mo-co_dimer.

R Fam; PF00173; heme_l; 1.

R Fam; PF00174; oxidored molyb; 1.

R PRINTS; PR00363; CYTOCHROMEB5.

R RINTS; PR00407; EUMOPTERIN.

R PROSITE; PS00191; CYTOCHROME B5. 1; 1.

R ROSITE; PS00191; CYTOCHROME B5. 2; 1.

R RASITE; PS00191; CYTOCHROME B5. 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
-i- CAUTION: It is not obvious if the molybdenum-pterin domain is functional; the conserved cysteine (position 339) is replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLYBDENUM-PTERIN DOWAIN (BY SIMILAROLYBDENUM-PTERIN DOWAIN (BY SIMILARON (HEWE AXIAL LIGAND) (BY SIMILAROLYBDENUM-PTERIN (BY SIMILAROLYBDENUM-PTERIN (BY SIMILAROLYB);
71ABID2B3465D811 (RCG4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ginetti F., Perego M., Albertini A.M., Galizzi A., "Bacillus subtilis mutS mutL operon: identification, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 1; Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROBABLE SULFITE OXIDASE. HEME-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=168;
MEDLINE=96349107; Pubmed=8760914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA mismatch repair protein mutl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence and mutagenesis.";
Microbiology 142:2021-2029(1996).
                                                                                                                                                                                              EMBL; AE003510; AAF48894.1; -. EMBL; AY069352; AAL39497.1; -. HSSP; P07850; 1SOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64346 MW;
                                                                                                                                                                                                                                                      FlyBase; FBgn0030966; CG7280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| :| | ||
503 QEEMPDGRHY 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 2
207 5
144 1
168 1
287 2
573 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.
                                      Ile-339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTL BACSU
P49850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTL_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
Manner V. Oggenera N. O. Montella B. Caphano V. Career S. M. Manner S. C. Oggenera N. O. Montella S. C. Theory S. M. Manner S. C. Oggenera N. O. Montella S. D. Montella S. Montella S. D. Montella S. Montella S. Montella S. Montella S. Montella S. Montella S. D. Montella S. D.
```

Search completed: December 22, 2003, 17:42:28 Job time : 5.6 secs

Run on:

```
ALIGNMENTS
029966
0922407
0802411
080282
080282
080282
0802811
095745
095745
095774
0961033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
0081033
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
008103
0081
                            December 22, 2003, 17:27:26 ; Search time 25.2 Seconds (without alignments) 112.642 Million cell updates/sec
                                                                                                                                                                                                                                                                                      830525
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                          sparches:
                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                  US-09-909-164-42
52
                                                                                                                                                                                 1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL
                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                    Perfect score:
                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                        Searched:
```

Q92hg7 streptococc Q864ul streptococc Q864ul streptococc Q885gl streptococc Q98xv4 streptococc Q98xv4 streptococc Q98xv4 streptococc Q96xv7 streptococc Q96xv7 streptococc Q96xv7 streptococc Q96xv7 streptococc Q96xv7 streptococc Q90xv1 anabaena sp Q81031 bos taurus Q81031 bos taurus Q8yvp1 anabaena sp Q8yvp1 anabaena sp Q8yvp1 anabaena sp Q8hxy9 bos taurus Q9yvp1 pasmodium Q95xk1 plasmodium Q94xk1 streptococc Q94xk3 streptococc Q94xy3 streptococc Q94xy3 streptococc Q94xy3 streptococc Q94xy3 streptococc Q94xy3 streptococc

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

unclassified:*

Database

BP_rvirus:*
BP_bacteriap:*

sp_archeap:*

SUMMARIES

| | Description | O8k289 mus musculu | Q46486 corynebacte | Q8cpj4 staphylococ | 040479 nicotiana t | Q91w50 nicotiana s | Q98hu6 rhizobium l | Q9x2e2 thermotoga | Q38317 lactobacill | 027679 methanobact | Q9elx6 cercopithec | Q8ime6 drosophila | Osyjii brucella me | Q8dih0 synechococc | Q9rxn9 deinococcus | Q9hlh8 thermoplasm | O16912 caenorhabdi |
|----|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| | | 08K289 | 16486 | 28CPJ4 | 240479 | 39LW50 | 298HU6 | 29X2E2 | 18317 | 327679 | 39B1X6 | 3 IME6 | 28YJ11 | Овріно | 29RXN9 | онтне | 16912 |
| | DB ID | 11 | Ö, | 16 | 91 | 10 | 16 | 16 | 9 | 11 | 12 | ō o | 16 | 16 | 16 | 17 | 2 |
| | Query Match Length DB | 413 | 208 | 1057 | 233 | 237 | 285 | 308 | 317 | 360 | 678 | 855 | 1028 | 1044 | 279 | 322 | 495 |
| مد | Query Match | 78.8 | 69.2 | 69.3 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 67.3 | 65.4 | 65.4 | 65.4 |
| | Score | 41 | 36 | 36 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 34 | 34 | 34 |
| | Result No. | 1 | 2 | 3 | 4 | S | 9 | 7 | 00 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |

| QBKSB9; 01-OCT-2002 (TERMELRE]: 22, Created) 01-OCT-2002 (TERMELRE]: 22, Last sequence update) 01-MAR-2003 (TERMELRE]: 23, Last sequence update) 01-MAR-2003 (TERMELRE]: 23, Last annotation update) Similar to expressed sequence A1987856. 1110004B19RIK. Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi; ROBI TAXID=10090; [1] SEQUENCE FROM N.A. Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; Submitted (JUN-2002) in | QBKR89; QBKR89; Q1-OCT-2002 (TEMBLI, Q1-OCT-2003 (TEMBLI, Q1-OCT-2003 (TEMBLI, Q1-OCT-2003 (TEMBLI, Q1-OCT-2003 (TEMBLI, Q1-OCT-2003 (TEMBLI, Q1-OCT-2003 (TEMBLI, Q1-OCT-2003 (Mouse) Mus musculus (Mouse) Musmalla; Mutazoa; Musmalla; Mutazoa; Musmalla; Mutazoa; Musmi, MC019195; AAH MGD; MG1:1915724; 11 SEQUENCE 413 AA; Query Match Q1:1915724; 11 Q1:191724; 11 Q1:191724; 11 Q1:191724; 11 Q46486; PRELIMIN Q1-NOV-1996 (TEMBLI, Q1-NOV-1996 (TEMBLI) Q1-NOV-1996 (TEMBLI) Q1-NOV-1996 (TEMBLI) Q1-NOV-1996 (TEMBLI) | date) update) brata; Euteleostomi; Muridae; Murinae; Mus. J databases. ODS CRC64; 1; Length 413; 3; Indels 0; Gaps 0; |
|--|--|---|
| 01-OCT-2002 (TERMELRel. 22, Created) 01-OCT-2002 (TERMELRel. 22, Last sequence update) 01-OCT-2002 (TERMELRel. 23, Last sequence update) 01-MAR-2003 (TERMELRel. 23, Last annotation update) Similar to expressed sequence A1987856. 1110004BHJSRIK. Mus musculus (Mouse) Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TAXID=10090; [1] SEGUENCE FROM N.A. Strausberg R., Strausberg R., Strausberg R., Strausberg R., Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; MGD; MGI:1915724; 1110004B19Rik. SEQUENCE 413 AA; 46621 MY; A98BAIDC70CDA0D5 CRC64; BMGD; MGI:1915724; 111004B19Rik. SEQUENCE 7; Conservative 1; Mismatches 3; Indels 0; Gaps 1 ERVYPXGKHYS 11 | 01-OCT-2002 (TTEMBL) 01-WAR-2003 (TTEMBL) 01-WAR-2003 (TTEMBL) Similar to expressed Similar to expressed Mus musculus (Mouse) Bukaryota, Metazoa; Mammalia; Butheria; McBmralia; Butheria; SEQUENCE FROM N.A. SEGUENCE FROM N.A. SEGUENCE FROM N.A. SEGUENCE 413 AA; MGD; MGI:1915724; 13 MGD; MGG; MGI:1915724; 13 MGG; MGG; MGG; MGG; MGG; MGG; MGG; MGG; | арв |
| 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Similar to expressed sequence A1987856. 1110004B19RIK. Mus musculus (Mouse). Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmalais Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. (I) SRQUENCE FROM N.A. SRQUENCE A13 A3, 46621 MW; A9BBAIDC70CDA0D5 CRC64; SRQUENCE 413 A4, 46621 MW; A9BBAIDC70CDA0D5 CRC64; SRQUENCE 7; Conservative 1; Mismatches 3; Indels 0; Gaps 1 ERVVPXGXHYS 11 | 01-OCT-2002 (TrEMBL) 01-MR-2003 (TrEMBL) 01-MR-2003 (TrEMBL) 01.10004B19RK. Mus musculus (Mouse) Mus musculus (Mouse) Musmalia, Butheria; MCBI TaxID=10090; [1] SEGUENCE FROM N.A. Strausberg R.; Straus | арв |
| 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Similar to expressed sequence A1987856. 1110004B19RIK. Mus musculus (Mouse) Bukaryotes, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. NCBI_TaxID=10090; [1] SRQURNCE FROM N.A. Strausberg R.; Str | 01-MAR-2003 (TrEMBLA SIMILAR to expressed SIMILAR musculus (Mouse) Mammalais Bukaryota; Mesacas, Mammalais Butheria; NCBI_TAXID=10090; SEQUENCE FROM N.A. Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R. MGI:1915/24; JAMISEQUENCE 413 AA; Duery Match 413 AA; Duery Match 6413 AA; Local Similarity Astches 7; Conserva Astches Matches 7; Conserva Astches 7; Conserva Matches 7; Conserva Matches 7; Conserva Matches 7; Conserva Matches Matches 7; Conserva Matches Matches 7; Conserva Matches Matches 7; Conserva Matches Matches Matches Matches 7; Conserva Matches Match | . 8 đ |
| Similar to expressed sequence A1987856. 1110004B19RIK. Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ROBILARID=10090; [1] SEQUENCE FROM N.A. Strausberg R.; Strausberg R.; SUMMILTED (UN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; | Similar to expressed similar to expressed illoodelsylk. Mus musculus (Mouse) Bukaryota; Metazoa; Metazoa; Metazoa; Metazoa; Metazoa; Metazoa; Metazoa; Strausberg R.; Submitted (JUN-2002) EMBL; BC032195; AAHMOD; MGI:1915724; 113 SEQUENCE 413 AA; Juery Match 1 BEVVDXGXHYE 1 BEVDBLININ 1 BEVVDXGXHYE 1 BEVDBLINININININININININININININININININININ | . 80 de |
| 1110004919RIK. Mus musculus (Mouse). Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MCBI_TAXID=10090; [1] SEGURNCE FROM N.A. SEGURNCE FROM N.A. SERIAL/SOLD to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; MGD; MGI:1915724; 1110004819Rik. SEGURNCE 413 AA; 46621 MW; A9B8A1DC70CDA0D5 CRC64; MGD; MGI:1915724; 1110004819Rik. SEGURNCE 413 AA; 65.21 MW; A9B8A1DC70CDA0D5 CRC64; ABCOURCE 413 AA; 76621 MW; A9B8A1DC70CDA0D5 CRC64; SEGURNCE 7; Conservative 1; Mismatches 3; Indels 0; Gaps 1 REVYPXGXHYS 11 | 1110004B19RIK Mus musculus (Mouse) Rukaryota; Metazoa; Mammalia; Butheria; NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. Strausberg R.; Str | арв |
| Mus musculus (Mouse) Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1] SRQUENCE FROM N.A. Strausberg R.; Submitted (JUD. 2002) to the EMBL/GenBank/DDBJ databases. EMBL; BCG32195; AA313195.1; MGD; MGI:1915724; 1110004B19Rik. SRQUENCE 413 AA; 46621 MW; A9BBAIDC70CDA0D5 CRC64; Duery Match 78.8%; Score 41; DB 11; Length 413; Duery Match 78.8%; Score 41; DB 11; Length 413; Atches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 1 BRVVRGXHYS 11 1 | Mus musculus (Mouse) Bukaryota, Metazoa; Mammalla, Eutheria; NCBI_TaxID=10090; [1] [1] [1] [2] [3] [3] [4] [5] [5] [5] [6] [6] [6] [7] [7] [7] [8] [8] [8] [8] [8] [8] [8] [8] [8] [8 | . gg |
| Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalialia; Butherla; Rodentia; Sciurognathi; Muridae; Musinae; Mus. NCSI TAXID=10090; [1] SCIURDENCE FROM N.A. STRUBENCE FROM N.A. STRUBENCE FROM N.A. STRUBENCE R.; SUDMITTED (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; | Bukaryota; Metazoa; Mamalia; Butheria; MCBI_TaxiD=10090; [1] TaxiD=10090; [1] TaxiD=10090; [1] SQUENCE FROM N.A. SEGUENCE FROM N.A. SEGUENCE A13 AA; SEGUENCE 413 AA; SEGUENCE 413 AA; Duery Match atches 7; Conserve atches 7; Conserve [| . 80.00 |
| Mammalls, Butheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TAXID=10090; [1] SEGURNCE FROM N.A. SEGURNCE FROM N.A. SEGURNCE FROM N.A. SERIALS CO.2195; AAH32195:1; MGD; MGI:1915724; 1110004B19Rik. SEQUENCE 413 AA; 46621 MW; A9BRAIDC70CDA0D5 CRC64; MGD; MGI:1915724; 1110004B19Rik. SEQUENCE 413 AA; 76621 MW; A9BRAIDC70CDA0D5 CRC64; MGD; MGI:1915724; 1110004B19Rik. SEQUENCE 413 AA; 76621 MW; A9BRAIDC70CDA0D5 CRC64; AB\$ SEQUENCE 1 AB\$ | Mammalia; Butheria; NCBI TaxID=10090; NCBI TaxID=10090; NCBI Examination of Submitted (JUN-2002) EMBL; BC032195; AAH MGD; MGI:1915724; 11 BEQUENCE 413 AA; Duery Match Best Local Similarity Aatches 7; Conserva Aatches 7; Conser | арв |
| INCBL_TaxID=10090; | NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. Strausberg R.; Strausberg R.; Submitted (JUN-2002) EMBL; MGG11915724; JAH- MGD; MG11915724; JAH- MGD; MG11915724; JAH- SEQUENCE 413 AA; SEQUENCE 413 AA; Local Similarity atches 7; Conservanticles 7; | 13; 0; Gaps |
| 1] | 1] SEQUENCE FROM N.A. STREEL SEQUENCE FROM N.A. STREEL SUBDITION OF STREET | 13; 0; Gaps |
| SEGUENCE FROM N.A. SEGUENCE FROM N.A. STREAMSDETG R.; Submitted (JUN2-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; MGD; MGI:1915724; 1110004B19R1k. SEQUENCE 413 AA; 46621 MW; A9BRAIDC70CDA0D5 CRC64; DNeTY MARCH TR. 8**; SCOTE 41; DB 11; Length 413; Sest Local Similarity 63.6*; Pred: No. 2.1; Atches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 1 REVVEXCHYS 11 | SEGUENCE FROM N.A. Strausberg R., Strausberg R., Submitted (UIM-2002) to the EWEL/GenBank/DDBJ of EWEL; BC032195, AAH32195.1; MGD; MGI:1915724; 1110004819Rik. BEQUENCE 413 AA; 46621 MW; A988A1DC70CDA0D5 Duery Match 78.84; Score 41; DB 11; Autches 7; Conservative 1; Mismatches 3; Autches 7; Conservative 1; Autches 4; Autches 7; Conservative 1; Autches 4; Autches 7; Conservative 1; Conservativ | 13; 0; Gaps |
| Strausberg R.; Submitted (JUD-2002) to the EMBL/GenBank/DDBJ databases. EMUL; BCG32195; AAH32195.1; EMUL; BCG32195; AAH32195.1; MGD; MGI:1915724; 1110004B19Rik. SEQUENCE 413 AA; 46621 MW; A9BBA1DC70CDA0D5 CRC64; Duery Match 78.8%; Score 41; DB 11; Length 413; Best Local Similarity 63.6%; Pred. No. 2.1; Atches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 1 BEVVPXXXHX 11 | Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ or EMBL; BCG3195; AR12195.1; | 13; 0; Gaps |
| Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032195; AAH32195.1; MGD; MGI:1915724; 1110004819Rik. SEQUENCE 413 AA; 46621 MW; A9BBA1DC70CDA0D5 CRC64; SEQUENCE 413 AA; 46621 MW; A9BBA1DC70CDA0D5 CRC64; SUBMIT MACh 78 | Submitted (JUN-2002) to the EMBL/GenBank/DDBJ of EMBL, BC032195, AAH32195.1, AAH32195.1, BC032195, AAH32195.1, BC032195, MAGD, MGT, MGT, MGT, MGT, MGT, MGT, MGT, MGT | 13; 0; Gaps |
| EMBL; BC032195; AAH32195.1; MGD; MGI:1915724; 1110004B19R1k. SEQUENCE 413 AA; 46621 MW; A9B8A1DC70CDA0D5 CRC64; SEQUENCE 413 AA; 46621 MW; A9B8A1DC70CDA0D5 CRC64; Duery Match 18. | EMBL; BC032195; AAH32195.1; MGD; MGI:1915724; 1110004819Rik. BEQUENCE 413 AA; 46621 MW; A988A1DC70CDA0D5 Duery Match 78.84; Score 41; DB 11; 4atches 7; Conservative 1; Mismatches 1; Conservative 1; Mismatches 1; Conservative 1; Mismatches 1; Conservative 1; Mismatches 1; EEVVPXGXHYS 11 | 13; 0; Gaps |
| MGD; MGI:1915724; 1110004Bi9Rik. SRQUENCE 413 AA; 46621 MW; A9BBAIDC70CDA0D5 CRC64; Duery Match 78.8*; Score 41; DB 11; Length 413; Best Local Similarity 63.6*; Pred. No. 2.1; Atches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 1 BEVVPCKHYS 11 168 REIPPLGKHYS 178 | MGD; MGI:1915724; 1110004Bi9R1K. SEQUENCE 413 AA; 46621 MW; A9B8A1DC70CDA0D5 Duery Match 78.8%; Score 41; DB 11; Best Local Similarity 63.6%; Pred. No. 2.1; 4atches 7; Conservative 1; Mismatches 1 EEVVPXGXHYS 11 | 413; 18 0; Gaps |
| SEQUENCE 413 A3, 46621 MW; A9BBAIDC70CDA0D5 CRC64; Query Match 78.8%; Score 41; DB 11; Length 413; Best Local Similarity 63.6%; Pred. No. 2.1; Aatches 7; Conservative 1; Mismatches 1 BEVVPXGXHYS 11 | SEQUENCE 413 A4; 46621 MW; A988A1DC70CDA0DS | . 413; 18 0; Gaps |
| Query Match 78.8%; Score 41; DB 11; Length 413; Ast Local Similarity 63.6%; Pred. No. 2.1; Astches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 1 EEVVPXGXHYS 11 | Duery Match 78.8%; Score 41; DB 11; Autches 7; Conservative 1; Mismatches 3 1 EEVVDXGXHYS 11 168 EEIPPLGKHYS 178 Q46486 PRELIMINARY; PRT; 208 AA. Q46486 (TrEMBLE). 01, Last sequence update 01-NOV-1996 (TrEMBLE). 01, Last sequence update 01-NAV-1996 (TrEMBLE). 116; Last annotation update 10-NAV-1996 (TrEMBLE). 116; Last annotation updated. | Length 413; i; Indels 0; Gaps |
| 1 BEVVPXGXHYS : 168 BEIPPLGKHYS | 1 BEV 168 EBII 168 EBII 2486 246486 01-NOV-1996 01-NOV-1996 01-NOV-1996 10-NOV-1996 10-NOV-1996 | |
| 168 REIPPLGKHYS | 168 BEII. 168 CHI. 1486 GG4486 046486 01-NOV-1996 01-NOV-1996 01-NOV-1996 | |
| | SULT 2 Q46486 Q46486 046486, 01-NOV-1996 01-NOV-1996 | |
| | 046486; 046486; 01-NOV-1996 01-NOV-1996 | |
| Had | 01-NOV-1996 01-NOV-1996 01-MAR-2001 | |
| Q46486 PRELIMINARY; PRT; | 01-NOV-1996 01-NOV-1996 01-MAR-2001 | |
| Q46486 PRELIMINARY; PRT; | 01-NOV-1996 01-MAR-2001 HYDOThetical | • |
| Q46486 PRELIMINARY; Q46486; 01-NOV-1996 (TrEMBLrel. 01, | UI-MAR-2001 | date) |
| 046486; 046486; 01-NOV-1996 01-NOV-1996 | Lact total | update) |
| 046486 ; 046486 ; 01-NOV-1996 01-NOV-1996 01-MAR-2001 | aypomenter form | |

```
SEQUENCE FROM N.A.

MEDLINB-20399450; PubMed=10945353;

MEDLINB-20399450; PubMed=10945353;

MEDLINB-20399450; PubMed=10945353;

"Characterization of gene expression of NBRRPs, transcription factors of basic PR genes from Nicotiana sylvestris.";

EMBL; ABO16264; BAA97122.1; -.

EMBL; ABO16264; BAA97122.1; -.

HSSP; 080337; 2GCC.

InterPro; IPR001471; TF_ERF.

Fram; PF00087; AR2-domaIn; 1.

ProDom; PD001423; TF_ERF; 1.

SMART; SM0380; AP2; 1.

SEQUENCE 237 AA; 26243 MW; 01BC3REB51E46298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana sylvestris (Wood tobacco).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                              Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledona; core eudicota;
Asteridae; lamiida; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                        SEQUENCE FROM N.A.

C STRAIN=BY4; TISSUB=Leaf;
C STRAIN=BY4; TISSUB=Leaf;
MEDLINEs=92726459; Pubmed=7756828;
A Obme-Takagi M., Shinshi H.;
T "Ethylene-inducible DNA binding proteins that interact with an ethylene responsive element.";
Train-1826; BAA07324.1; -..
REMBL; D38126; BAA07324.1; -..
REMBL; D38126; BAA07324.1; -..
REMBL; D38126; BAA07324.1; -..
REMBL; D890141; TF ERF.
DR Ffam; PP00847; AP2-domaIn; 1.
ProDom; PD001423; TF ERF; 1.
SMART; SMO380; AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%; Score 35; DB 10; Length 233; 60.0%; Pred. No. 23; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Bthylene-responsive element binding factor.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.3%; Score 35; DB
60.0%; Pred. No. 23;
ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                           EREBP-2.
Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 QAVVPKGRHY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 BEVVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 QAVVPKGRHY 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4096;
                                                                                                                                                       NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09LW50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSMT60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSERF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9LW50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                   SPECIES=C.striatum, STRAIN=M82B;
MEDLINE=20194806; PubMed=10732668;
Tauch A., Krieft S., Kalinowski J., Puhler A.;
Tauch A., Krieft S., Kalinowski J.,
"The 51,409-bp R-plasmid pTP10 from the multiresistant clinical
isolate Corynebacterium striatum M82B is composed of DNA segments
incitally identified in soil bacteria and in plant, animal, and human
pathogens.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                       SPECIES—C.xerosis; STRAIN=M82B;
MEDIATRE=96177603; PubMed=8559800;
Tauch A., Kassing F., Kalinowski J., Puhler A.;
"The Corynebacterium xerosis composite transposon Tn5432 consists of two identical insertion sequences, designated IS1249, flanking the erythromycin resistance gene ermCX.";
Plasmid 34:119-131(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterinea; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL; ABOLG746; AAO04476.1; -. Complete proteome. EMBC 2007 BAB 201674 BAB 2017391 MW; 8944D7D8DB1CAES9 CRC64; SEQUENCE 1057 AA; 117391 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Gen. Genet. 263:1-11(2000).

EMBL; U21300; AAC95478.1; -.

EMBL; AF024666; AAG03300.1; -.

Hypothetical protein; Plasmid.

SEQUENCE 208 AA; 23012 MW; PIS04BEIECDE85A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSCPJ4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Carbamoyl-phosphate synthase large chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.2%;
50.0%;
        Corynebacterium xerosis, and Corynebacterium striatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 63.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 KEVVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|:| | ||:
130 DVIPEGKHYA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     040479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8CPJ4
```

Matches

ઠ g

RESULT 3

Q8CPJ4

ö

Gaps

ö

ö

Gapa

ö

233 AA

PRT;

PRELIMINARY;

RESULT 4

ઠે

Q40479

```
PRINTS; PR00721; STOMATIN.
SWART; SM0244; PHB; 1.
Procease; Complete proteome.
SRQUENCE 308 AA; 34778 WW; ADE03603E5101A9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=12417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (
01-NOV-1996 (
01-MAR-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                           Q38317
                                                                                                                                                                                                                                                                         RESULT 8
   8 4 8 8
                                                                                                                                                                          8
                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                 MEDLINE=21082930; PubMed=11214968;

MEDLINE=21082930; PubMed=11214968;

Maneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

Hatanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T.,

Mishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

Takeuchi C., Yamada M., Tabata S.;

Tomplete genome structure of the nitrogen-fixing symbiotic bacterium of the sorbizobium loti.";

DNA Res 7.331-338(2000).

EMBL; AP003000; BAB49770:1;

InterPro; IPR002345; Cytc heme_bind.

InterPro; IPR002345; Cytc Cheme_bind.

InterPro; PR00180; Cytcchrome C1:

PR PRINTS; PR00603; CYTOCHROWEC1.

PROSITE; PS00190; CYTOCHROWEC1.

PROSITE; PS00190; CYTOCHROWEC2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                      Rhizobium loti (Megorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Megorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%; Score 35; DB 16; Length 285; 55.6%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 AA; 30961 MW; 31D9CDE2711747EE CRC64;
                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
FTSH protease activity modulator HFLK.
                                         285 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001107; Band 7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band 7; 1.
                                                                           01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 VIPEGTHYN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 WPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                         STRAIN=MAFF303099;
                                                                                                                                                                                                                         NCBI_TaxID=381;
                                                                                                                                  Cytochrome c1.
MLL2705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                             098HU6;
                                       098HU6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9X2E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
RESULT 6
Q98HU6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9X2E2
                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DA PURE PRESENTA PROSECTION OF STREET PROSECTION OF
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fremaux C., De Antoni G., Raya R., Klaenhammer T.; "Genetic organization and sequence of the region encoding integrative functions from Lactobacillus gasseri temperate bacteriophage phi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Engel G., Altermann E., Klein J., Henrich B.;
"Structure of a genome region of the Lactobacillus gasseri temperate phage phi add covering a repressor gene and cognate promoters.";
Gene 210:67-70(1998).
EMBL; AJ131519; CAB52540.1;
InterPro: IPR002653; Glyco-hydro-25.
InterPro: IPR003646; SN3 bac.
Pfam; PR01183; Glyco-hydro-25; 1.
Probon; PD004620; Glyco-hydro-25; 1.
Probon; PD004620; Glyco-hydro-25; 1.
SMART; SM00641; Glyco-25; 1.
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINB=99384014; PubMed=10452953;
Altermann B., Klein J., Henrich B.;
Prinary structure and features of the genome of the Lactobacillus gasseri temperate bacteriophage phi-adh.";
Gene 236:333-346(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactobacillus bacteriophage phi adh.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99138034; PubMed-7836307;
Henrich B., Binishofer B., Blaesi U.;
"Frihary structure and functional analysis of the lysis genes
Lactobacillus gaseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
  Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 35; DB 9; Length 317; 66.7%; Pred. No. 32; ive 1; Mismatches 2; Indels
                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Altermann E.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 AA; 34703 MW; 9FF2715EB43561C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
67.3%; Score 35; DB 16; 75.0%; Pred. No. 31;
                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93231538; PubMed=8472961;
                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 01, C
(TrEMBLrel. 01, L
(TrEMBLrel. 23, L
Query Match
Best Local Similarity 75.0
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66.7
Matches 6, Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 126:61-66(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 WPXGXHYS 11
                                                                                                      3 WPXGXHY 10
                                                                                                                                                      41 WPSGIHY 48
```

50.0%;

60 VVPMGYHYA 68

셤

```
MEDLINE=98037514; PubMed=9371463;
MEDLINE=98037514; PubMed=9371463;
Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
Daniani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
Complete Sequence of the Simian Varicella Virus Genome.";
Submitted (WAR-2011).

EMBL, AF275348; AAG27217.1;
Hypothetical protein.

SEQUENCE 678 AA; 75850 MW; A17B09E30512FE3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                             Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155 (1997).
REMBL; AR000923; AAB86115.1;
RINEEPRO; IPR005140; eRF1_1.
RINEEPRO; IPR005141; eRF1_2.
RINEEPRO; IPR005141; eRF1_3.
RINEEPRO; IPR004045; Pell.
Refam; PF03463; eRF1_1; 1.
Refam; PF03464; eRF1_2; 1.
Refam; PF03464; eRF1_2; 1.
Refam; PF03465; eRF1_3; 1.
Refam; PF03465; eRF1_3; 1.
Refam; PF03465; eRF1_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%; Score 35; DB 17; Length 360; 45.5%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12; Length 678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell division, Complete proteome.
SEQUENCE 360 AA; 40814 MW; 2A000CB4B3CEF469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecine herpesvirus 7.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NIBI TaxID=35245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 75.9 kDa protein.
                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35;
                                                                                                                                                                                                                                                                                Methanobacterium thermoautotrophicum.
                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%;
                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGXHYS 11
                                                                                                                                                                                                                        Cell division protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                  MTH1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9E1X6
Q9E1X6;
                                                                                           027679;
                                                       027679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
                             027679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9E1X6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOT THE REAL REAL OF THE PARTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
RR MINE-20196065; PubMed-10731132;

RR MEDINE-20196065; PubMed-10731132;

RA Adams M. D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M. D., Celniker S.E., Richters S. Mablurner M., Henderson S.N.,

RA Adams M. D., Celniker S.E., Richters S. Mablurner M., Henderson S.N.,

RA Button G.G., Mortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,

Ratchon R.C., Rogers Y.H., Blazzej R.G., Nalson C.R., Gabor G.L.,

RA Beson K.Y., Besne P.V., Bazzej R.G., Nalson C.R., Gabor G.L.,

RA Beson K.Y., Basu A., Baxendala J., Bayerakazoglu L., Besaley B.M.,

Ratchova D., Botchan M.R., Buutler H., Cadleu B., Brindari D., Bolhhakov S.,

Rockova D., Botchan M.R., Buutler H., Cadleu B., Center A., Chandra I.,

RA Buttis R.C., Busam D.A., Buller H., Cadleu B., Britaler P., Brottler P.,

RA Buttis R.C., Busam D.A., Balke C., Davemport L.B., Davies P.,

Ra Dodoon K., Doup L.B., Downes M., Dayan-Rocha S., Dunkov B.C.,

RA Buttis R.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Hurris N.L., Harvey D., Heiman T.J., Weil M.H., Ibogwam C.,

RA Hostin D., Houston K.A., Heiman T.J., Weil M.H., Ibogwam C.,

RA Hostin D., Houston K.A., Mowland T.J., Weil M.H., Ibogwam C.,

Rabor R., Kalush P., Karpen G.H., Kez Z., Kennigon J.A., Ketchum K.A.,

Rabon R., Kalush P., Karpen G.H., Kez Z., Kennigon J.A., Ketchum K.A.,

Rabon R., Moy M., Murphy B., Murphy L., Murphy L., Murph, J., Murph, J.,

Rollen B.R., Rodina C.D., Stapen M., Stupski M. P., Sacleb J.M.,

Rabon D.R., Nelson K.A., Nixon K., Musskern D.R., Pacleb J.M.,

Rabon B.C., Siden-Kiamos I., Simpson M., Strong X., Yao Q.A., Ye J.,

Rabon R., Tector C., Thurer R., Venter B., Wang A.,

Rabor R., Tector C., Thurer R., Venter B., Wang A.,

Rabor R., Tector C., Thurer R., Venter B., Wang A.,

Rabon R.M., Wassarman D.A., Weither B., Wang A., Walliams S.M., Woodager, Waller B.C., Stapheron M., Strong R.,

Rabon R.M., Walsen R.M., Rodon W., Zhong W., Zhon G., Zheng L.,

Rabon R.M., Walser R.M., Rodon R.M., Wang G., Zhon W., Walber R.,

Rabon R.M., Walser R.M., Rodon R.M., 
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Celniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Bayas C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,
Perriera S., Frise E., Galle R.P., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
                      ö
                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Hakapoda; Insecta; Pterygota;
Neoptera; Brooptery; Diptera; Brachycera; Muscomorpha;

Bphydroidea; Drosophilidae; Drosophila.
                      Indels
                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                      3,
                                                                                                                                                                                                                   855 AA
Pred. No. 72;
2; Mismatches
                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                (TrEMBLrel. 23, (TrEMBLrel. 23,
                      Conservative
                                                                                                                                                                                                               PRELIMINARY;
                                                                                         147 BRIIPKGTRY 156
                                                                1 BEVVPXGXHY 10
Best Local Similarity
Matches 5, Conserv
                                                                                                                                                                                                                                                                                01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                        CG30437-PC.
                                                                                                                                                                                                                                                                                                                                                CG30437
                                                                                                                                                                                                                 Q8 IMB6
                                                                                                                                                                         RESULT 11
                                                                                                                                                                                           ò
                                                                                                      셤
```

```
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Praser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9RXN9;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=R1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                              Q8DIH0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9RXN9
                                                       Matches
                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                     ОВБІНО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RXN9
                                                                                                            Š
                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=16M / ATCC 23456 / Biotype 1;
STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
MEDLINE=20020109; PubMed=11756688;
MINIOTICALIO V.G., Kapatral V., Redar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman B., Selkov E., Bizer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Hagelkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                        Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B., Tupy J.L., Bergman E., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Milburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield B., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.; Shubrited (MAR-2000) to the EMBL/GenBank/DDBJ databases.
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Paragas V., Park S., Patel S., Pfelifer B., Photanenavons S., Pittman G.S., Puri V., Richards S., Scheeler P., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Rubin G.M.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 5; Length 855;
Pred. No. 93;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete protecome. - - - SEQUENCE 1028 AA; 112996 MW; A752B7042572E219 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003786; AAN16124.1; -.
SEQUENCE 855 AA; 94532 MW; 39BD5A516D6312DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AB009470; AAL51457.1; -
InterPro; IPR0012086; Aldehyde_dehydr.
InterPro; IPR001410; DBAD.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1028 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00490; HELICC; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR 2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23, ATP-dependent DNA helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||| | |
657 DEVVPSGDH 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BEVVPXGXH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brucella melitensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBаве;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08YJ11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8YJ11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            datches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          087311
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SO DE REPARENTE DE LA PACE DE LA
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White O., Eisen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchm K.A., Nelson K.B., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasamoto
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamotc Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 16; Length 1044;
Pred. No. 1.2e+02;
1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001889; AAF09867.1; -.
Score 35; DB 16; Length 1028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
WCBI_TaxID=1299;
                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
                                                                                                                                                                                                                                                                                                                                                           Synechococcus elongatus (Thermosynechococcus elongatus).
                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Cyanobacteria, Chroococcales, Synechococcus
                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                  Pred. No. 1.1e+02;
2; Mismatches 3
                                                                                                                                                                                                                     PRT; 1044 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created) (TrEMBLrel. 13, Last seq (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BP-1;
MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AP005374; BAC09170.1; -. Complete proteome.
                                                                                                                                                                                                                                                                                                                      Multidrug efflux transporter.
    67.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.68;
                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein DR0271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6.
Local 7; Conservative
                                         6; Conservative
                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:| | ||
843 EEVLPNGIGYS 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                              1 EEVVPXGXHYS 11
                                                                                                        |::|| | ||
76 EKIVPPGARYS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 BEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 9:123-130
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BEQUENCE FROM N.A.
```

```
ö
                                                            ö
                                                                                                                                                                                                                                                                  Gaps
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels
                                       Query Match 65.4%; Score 34; DB 16; Length 279; Best Local Similarity 75.0%; Pred. No. 46; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                         Thermoplasma acidophilum.
Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=2303;
TIGR; DR0271; -. Hypothetical protein; Complete proteome. SEQUENCE 279 AA; 31140 MW; DCEA100E0AEE8831 CRC64;
                                                                                                                                                            OSHLHB;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Glucose-fructose oxidoreductase related protein.
                                                                                                                                                      322 AA
                                                                                                                                                     PRT;
                                                                                                                                                     PRELIMINARY;
                                                                                                   100 VPLGRHYS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGXHY 10
                                                                                4 VPXGXHYS 11
                                                                                                                                                     9нгн60
                                                                                                                               RESULT 15
Q9HLH8
                                                                                  δ
                                                                                                   q
                                                                                                                                                               ઠે
```

Search completed: December 22, 2003, 17:51:31 Job time : 26.2667 secs

66 WPDGLHY 73

g

Hepatitis C virus

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

```
/note= "Norvalyl carbonyl forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide,
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
/note= "C-terminal amide"
          ABB80535
ABB80536
ABB80559
ABB80559
ABB80564
ABB80565
ABB80566
ABB80566
ABB80566
ABB80566
ABB80566
ABB80551
ABB80551
ABB80534
ABB80555
ABB80556
ABB80556
ABB80556
                                                                                                                                                                                                                                                                                                                            ABB80523
ABB80527
ABB80531
ABB80532
ABB80532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB80544 standard; peptide; 11 AA.
 21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
  W0200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
  ABB80544;
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
ABB80544
 Hepatitis C virus Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    December 22, 2003, 16:41:00 ; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec
                                                                                                                                                                                                                                                                                                   A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                            1107863
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                       1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB80544
ABB80549
ABB80552
ABB80553
ABB80553
ABB80521
ABB80522
ABB80522
                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
                                                                                                             US-09-909-164-43
48
                                                                                                                                    1 EEVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.8
93.8
93.8
93.8
93.8
91.7
91.7
```

Score

Result No.

Gapa

ö

DB 23; Length 11;

0.011;

Score 45; DB 2 Pred. No. 0.011 0; Mismatches

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of
                                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB80549 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 65; 69pp; English.
                                          Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunck
                                                                                                                                                                                                                                                                                                93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                1 BEVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                               BEVVPXGTSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Levy OB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
  virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80549;
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus, HCV, serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                            peptide compound having hepatitis C virus protease inhibitory ty useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 23;
Pred. No. 0.011;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB80545 standard; peptide; 11 AA.
                                          Brunck TK;
                                                                                                                                                                                                                Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 90.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 REVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ,
  (CORV-) CORVAS INT INC
                                            Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-361643/39.
                                                                                    WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lim-wilby M, Levy
                                                                                                                                                                                                                                                                                                                                                                                                                               11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                        virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                          Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80545,
                                                                                                                              Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
ABB80545
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
```

Ŧ,

```
Conservative
 10;
                                                                                                                     08-OCT-2002
                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
                                                                                                                                                                                     Synthetic.
                                                                                                    ABB80553;
                                                                                                                                                                    virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
 Matches
                                                                 RESULT 5
                                   셤
                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
           ingredient
                                                                                                                                                                                                                                                                                                                   "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                          Gaps
                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingris useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #32
                                                                          ö
                                                                         1; Indels
                                                       Length
                                                     Score 45; DB 23;
Pred. No. 0.011;
); Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 23;
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                  note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                 "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                               note= "D-form residue"
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ϋ́
                                                                                                                                                          ABB80552 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 65; 69pp; English
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunck
                                                      93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                              (first entry)
                                                                        10; Conservative
                                                                                          1 EEVVPXGXSYS 11
                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levy OE,
                                                                                                            BEVVPXGSSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-361643/39.
                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                    11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AA;
                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus protease
                                                                                                                                                                                                                                                                                                                                                                                   WO200208251-A2
                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lim-wilby M,
                                                                                                                                                                                              08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                                                                                                                                                                                              Synthetic
                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel per
activity
                                                       Query Match
                                                                                                                                                                                                                                             virucide
                                                                        Matches
SKSSS
                                                                                          ઠે
                                                                                                           g
```

Length 11;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredits useful for treating disorders associated with hepatitis C virus.
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #33.
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.8%; Score 45; DB 23; Length 11; 90.9%; Pred. No. 0.011; ive 0; Mismatches 1; Indels
Indela
;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 65; 69pp; English.
ö
                                                                                                                                                                                                  ABB80553 standard, peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                            BRVVPXGXSYS 11
                                                                                    REVVPXGSSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 REVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEVVPXGSSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 10, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

us-09-909-164-43.rag

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                       /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                            compound having hepatitis C virus protease inhibitory
il for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 23; Length 11;
Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                  note= "N-terminal acetyl"
                                                                                                                                                                                        /note= "C-terminal amide"
                                                                                                                                                                /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1
                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80525 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%;
                                                                                                                                                                                                                                                                                          21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 REVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
                                                                                                                                                                                                                                                                                                                                            Levy OE,
                                                                                                                                                                                                                                                                                                                   (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                             peptide con
                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                 MO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                        virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                          Key
Modified-site
                                                                                                             Modified-site
                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                            Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-2002
                                                                                                                                                                                                                                         31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virucide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                          virucide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha *ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                     "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%; Score 44; DB 23; Length 11; 90.9%; Pred. No. 0.018; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                              'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                               11
/note= "C-terminal amide"
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŢĶ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80522 standard; peptide; 11 AA.
                                   ABB80521 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunck
                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGXSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEVVPXGMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease
                                                                                                                                                                                                                                                                                                                   WO200208251-A2
                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-2002
                                                                                    08-OCT-2002
                                                                                                                                                                                                                                                                                                                                             31-JAN-2002
                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                              ABB80521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
           RESULT 6
                       ABB80522
```

ô

Gaps

ö

셤

ઠે

#XXXX

```
21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                1 REVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
/note=
                                                                                                                       Levy OE,
                                                                                                     (CORV-) CORVAS INT INC
                                                                                                                                          WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                               11 AA;
                           WO200208251-A2
Modified-site
                                                                                                                                                                                virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                       Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80530;
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
셤
                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                         The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                 /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                       91.7%; Score 44; DB 23; Length 11; 90.9%; Pred, No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
/note= "N-terminal acetyl"
                                                                /note= "C-terminal amide"
                                             'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80526 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                       Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                Brunck
                                                                                                                       19-JUL-2001; 2001WO-US23169
                                                                                                                                          21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                                                                                Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                            EEVVPXGMSYS
                                                                                                                                                                                                 WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
ses 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 9
                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                     Misc-difference
                                                                                                                                                                                                                                        virus protease
                                                                                  WO200208251-A2
                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                             Lim-wilby M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-2002
                                                                                                    31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80526;
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virucide.
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80526
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                              g
8
```

```
/note= "Norvalyl carbonyl forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 23; Length 11;
Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
11
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80530 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%;
                                                                                                                                                                                                                                   19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                              21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001, 2001WO-US23169
```

```
Claim 17; Page 64; 69pp; English.
                                                                                                                                                             1 BEVVPXGXSYS 11
                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lim-wilby M, Levy OE,
                                                                                                                                                                                1 REVVPXGQSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 9
                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                      08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2002
                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                   ABB80536;
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                    virucide.
                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                          $$$$$$$$$$$$$$$$
                                                                                                                                                               ò
                                                                                                                                                                              셤
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #15.
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                       Score 44; DB 23; Length 11;
Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brunck TK;
                             Brunck TK;
                                                                                                                                                                                                                                                                                                                               ABB80535 standard; peptide; 11 AA.
                                                                                                       Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                       91.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                               Local Similarity 90.
                                                                                                                                                                                                                                                             1 REVVPXGXSYS 11
                                                                                                                                                                                                                                                                               REVVPXGGSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lim-wilby M, Levy OE,
                             Lim-wilby M, Levy OB,
          (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4PI; 2002-361643/39
                                                WPI; 2002-361643/39
                                                                                      virus protease -
                                                                                                                                                                                                    11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                     08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                  ABB80535;
                                                                                                                                                                                                                                                                                                                                                                                                                     virucide.
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                      ABB80535
                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                               셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoomide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with NCV proteasse. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #16
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                              Score 44; DB 23; Length 11;
Pred. No. 0.018;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB80536 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunck
                                                                                                                                                                                                                                                                                                                                                             91.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.9
Matches 10; Conservative
```

11

Ħ

```
BEVVPXGOSYS
         REVVPXGXSYS
                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-2000;
                                                                                                                  08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                         31-JAN-2002
                                                                                                                                                                                      Synthetic
           -
                                                                                                ABB80540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                   virucide
                                                         RESULT 14
                          셤
                                                                             ð
           δ
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV procease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                           /note= "Norvaly1 carbonyl forming keto-amide linkage with
    residue 7"
pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                  Gaps
                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #19.
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%; Score 44; DB 23; Length 11; 90.9%; Pred. No. 0.018; ive 0; Mismatches 1; Indels
                                                DB 23; Length 11;
                                                                 1; Indels
                                               Score 44; DB 23;
Pred. No. 0.018;
0; Mismatches
                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                         'note= "D-form residue"
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                          ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brunck TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 65; 69pp; English.
                                                                                                                                                        ABB80539 standard; peptide; 11
                                              91.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-220101P
                                                                                                                                                                                               (first entry)
                                           Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                 EEVVPXGQSYS 11
                                                                                     1 EEVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                              Misc-difference 8
                           11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AA;
                                                                                                                                                                                                                                                                                                                                                                                               WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus protease
                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lim-wilby M,
                                                                                                                                                                                               08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2002
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                            ABB80539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                            Sequence
                                                                                                                                       RESULT 13
ន្តដូល
                                                                                                                                                                            ઠ
                                                                                                        셤
```

ö

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                             "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ingredient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketoanide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture is medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredits useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 23; Length 11
Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                               'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
  Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŢĶ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
ABB80540 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brunck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-220101P.
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 REVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVVPXGQSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus protease
                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                            /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%; Score 44; DB 23; Length 11; 90.9%; Pred. No. 0.018; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                     /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                              /note= "C-terminal amide"
                                                                                                                                                                                                                                                                       'note= "D-form residue"
                                                                                                                                                                                                                                                                                                /note= "Oxymethionine"
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brunck TK;
ABB80559 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2000; 2000US-220101P.
                                                   08-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AA;
                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                          WO200208251-A2
                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002.
                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                      ABB80559;
```

Search completed: December 22, 2003, 17:41:02 Job time : 32.4667 sec8 1 REVVPXGMSYS 11 ద

ô

Gaps

ö

Best Local Similarity 90.9 Matches 10, Conservative

1 EBVVPXGXSYS 11

ઠે

٠,

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-637-759B-236
RESULT 1
Sequence 236, App
Sequence 236, App
Sequence 236, App
Sequence 4, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 27, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7885, Ap
68, Appl
11, Appli
11, Appli
359, Appli
2, Appli
2, Appli
220, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                 December 22, 2003, 16:37:03 ; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seduence Sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                           328717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*

( / cgn2 / fytodata/1/laa/5A COMB.pep:*
): / cgn2 / fytodata/1/laa/5B COMB.pep:*
): / cgn2 / fytodata/1/laa/6A COMB.pep:*
): / cgn2 / fytodata/1/laa/6B COMB.pep:*
): / cgn2 / fytodata/1/laa/PCTUS COMB.pep:*
): / cgn2 / fytodata/1/laa/PCTUS COMB.pep:*
): / cgn2 / fytodata/1/laa/PCTUS COMB.pep:*
                  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-637-759B-236
US-08-871-355A-236
US-09-221-945-236
US-09-221-945-236
US-09-221-945-236
US-09-1018-211-4
PCT-US91-0211-4
US-09-152-06-6
US-09-152-06-6
US-09-152-06-8
US-09-152-06-8
US-09-152-06-8
US-09-152-06-8
US-09-152-06-8
US-09-153-08-1
US-09-96-243-359
US-09-96-243-359
US-09-961-083-220
US-09-961-083-280
                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                    328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 2000000000
                                                                                                                                                                                                              US-09-909-164-43
48
                                                                                                                                                                                                                                                     1 EBVVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ........
                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                             OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
```

```
Appli
                                                                                                               Sequence
Seq
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/637,759B

FILING DATE: 03-MAY-1996

CLASSIFICATION NUMBER: PCT/0895/02875

PILING APPLICATION: 435

ATYONEY/AGENT INFORMATION:

NAWE: Pabest, Patrea L.

REGISTRATION NUMBER: 31,284

REGISTRATION OF SEO ID NO: 236:

BEQUIENCE CHARACTERISTICS:

LEMOTH: 45 amino acids

LEMOTH: 45 amino acids

LEWOTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 236, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSES: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: ADDRESSES:
CITY: Atlanta
STREET: USA
COUNTRY: USA
US-08-361-517-19
PCT-US93-07964-19
US-08-440-861-53
US-07-940-861-53
US-08-175-096-8
US-09-047-125-27
US-09-047-125-27
US-08-413-974-4
US-08-413-974-4
US-08-413-974-4
US-08-413-974-6
US-08-413-288-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 2;
Pred. No. 8.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%; Scut.
60.0%; Pred
1;
       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-236
```

ö

Gaps

ö

Indela

셤

ઠે

```
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT PPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 32; DB 4; Length 947; 66.7%; Pred. No. 2.4e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 32; DB 4; Length 45; 60.0%; Pred. No. 8.3; tive 1; Mismatches 3; Indels
                                                ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30

CURRATT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-228-986-73
; Sequence 73, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404,873-8734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 BEVVPXGXSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ERISPLGWSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686 VMPSGISYS 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGXSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
Georgia
                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-201-945-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-08-844-086-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 3; Length 45;
Pred. No. 8.3;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: REALABLE FORDS

COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PRE-BLID PC-DOS/MS-DOS
SOFTWARE: PARE-BLID NUMBER: US/08/871,355A
FILING DATE: US/08/871
FIL
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Parrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
CONVIRK: USA
ZIP: 30199-3450
ZIP: 30199-3450
ZIP: 30199-3450
ZIP: MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 236, Application US/09201945
Fatent No. 6342215
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
TADDRESSES: Patrea L. Pabst
STREET: 2800 One Allantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                 US-08-871-355A-236
; Sequence 236, Application US/08871355A;
; Patent No. 6015669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||: | | ||
ERISPLGWSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGXSY 10
EEVVPXGXSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-201-945-236
```

ઠે 셤

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US91-02714-26

Sequence 26, Application PC/TUS9102714

GENERAL INFORMATION:

APPLICANT: Wichael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related TITLE OF INVENTION: Processes

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray & ADDRESSER: Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
64.6%; Score 31; DB 3; Length 159;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIFICATION NUMBER: BCT/US91/02714
FILING DATE: 20-APR-1990
ATTONEY/AGENT INPORMATION:
NAME: BOLUN, Michael F:
REGISTRATION NUMBER: 25447
REGISTRATION NUMBER: 25447
REGISTRATION NUMBER: 25447
TELECOMMUNICATION NUMBER: 27805/30197
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAKE. (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,086
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9607993.4
APPLICATION NUMBER: 9607993.4
ATTORNEY/AGENT INFORMATION:
NAMB: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
TELEPHONE: 610-270-4478
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
FYPE: amino acids
FYPE: amino acid
FYPE: amino acid
FYPE: single
FYPE: protein
US-09-018-211-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (312) 346-5750
TELEPAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEG ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 EEVLPDGTS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 BEVVPXGXS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 2; Length 159;
Pred. No. 53;
1; Mismatches 2; Indels
Sequence 4, Application US/08844086
Patent No. 5866390
GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5866390el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: 709 Swedeland Road
CITY: King of Prussia
STREET: 709 Swedeland Road
CITY: Ring of Prussia
STREET: PA
                                                                                                                                                                                                                                                                               COUNTY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
APPLICATION NUMBER: USA
APPLICATION NUMBER: 9607993.4
FILING DATE: IS-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: B3,891
TELEPHONE: G10-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09018211
Patent No. 6048716
GENERAL INPORMATION:
AND SEQUENCES:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKiine Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STREET: POS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TEM Compatible
COMPUTER: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.6%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-844-086-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 EEVLPDGTS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 REVVPXGXS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-09-018-211-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
31 REVVPAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEVVPXG 7
                                                                                                                                                                                                                                                                                                                           07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-688-352C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08459146

Patent No. 5866405

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Genetically Engineered Transmissible

TITLE OF INVENTION: Hypovirulence

TITLE OF INVENTION: Hypovirulence

NUMBER OF ENGUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street

CTIT: New Jersey

COUNTRY: U.S.A.
                                                                                                                    Score 31; DB 5; Length 513;
Pred. No. 1.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 2; Length 622; Pred. No. 2.4e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: 02-UN-1995
FLING DATE: 02-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FRB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: parasitica)
STRAIN: RP713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ROBEMEN, CALHETINE R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8589
TELECOMMUNICATION INFORMATION:
TELEFAN: (201) 235-6208
TELEFAN: (201) 235-5500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.6%;
85.7%;
                                                                                                                      Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 622 amino acids
amino acid
LENGTH: 513 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                          201 WPAGGSY 208
                                                                                                                                                                                                      3 WPXGXSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 EEVVPAG 37
                                                                              PCT-US91-02714-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-459-146-2
                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-459-146-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
| Use | Use
```

Gaps

```
US-09-146-249A-28

US-09-146-249A-28

US-09-146-249A-28

SEQUENCE 28, Application US/09146249A

PATENT No. 6069240

GANERAL INFORMATION:

APPLICANT: Wigler, Michael H.

TITLE OF INVENTION: Cloning by Complementation and Related

TITLE OF INVENTION: Processes

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun STREFT: 6100 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

CONTRY: United States of America

ZIP: 60606-6402

COMPUTER: READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/146,249A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31, DB 2; Length 688;
Pred. No. 2.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.6%; Score 31; DB 3; Length 688; 75.0%; Pred. No. 2.7e+02;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/688,352

FILING DATE: 19-ARR-1991
ATTORNEY/AGEN: INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
IREPRENCATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
ILENGTH: 688 amino acide
ITYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: Amino acide
TYPE: Information Topology: 11 near

NOLECULE TYPE: protein
US-08-474-379C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
PILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTATION NUMBER: 36,107
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-146-249A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 WPAGGSY 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VVPXGXSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WESULT 11
US-08-474-379C-28
Sequence 28, Application US/08474379C
Sequence 28, Application US/08474379C
Sequence 28, Application US/08474379C
Sequence 28, Application US/08474379C
SEGUENT COLONIOS
SEGUENCE COLOCALIA, John J.
TILE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
NUMBER: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STRET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STRET: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COUNTRY: United States of America
COUNTRY: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: US/08/474,379C
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING DATE: US/08/474,379C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUGTWARE: Patentin Release #1.0, Version #1.25
SUGTWARE: Patentin Release #1.0, Version #1.25
SUGTRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 10-APR-1990
ATTORNEY AGENT INFORMATION:
PILING DATE: 20-APR-1990
ATTORNEY AGENT INFORMATION:
TELECOMMUNICATION OFFICE:
SEQUIENCE: 688 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 1; I
Pred. No. 2.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.6%;
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11near
MOLECULE TYPE: protein
US-07-688-352C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 WPAGGSY 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VVPXGXSY 10
                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```